



20010-04USA.ST25

SEQUENCE LISTING

<110> POSCO
POSTECH
An, Gynheung
Ryu, Choong-Hwan
Han, Jong-Jin
Kang, Hong-Gyu
An, Kyungsook

<120> ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
MUTAGENESIS OF RICE

<130> 20010-04USA

<140> US 10/713,648

<141> 2003-11-14

<150> 60/427,166

<151> 2002-11-15

<160> 83

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 474

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (394)...(474)

<223> segment of the T-DNA insert in line 1B-115-22

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<213> Oryza sativa

<220>

<221> misc_feature

<222> (104)...(194)

<223> segment of the T-DNA insert in line 1B-164-43

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<210> 3

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<211> 325
 <212> DNA
 <213> Oryza sativa
 <220>
 <221> misc_feature
 <222> (255)...(325)
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 tgtaggaggc aacttcctag aggggaagtat tccacaatca ttagcaaatc tcagggggcac 180
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<210> 4
 <211> 650
 <212> DNA
 <213> Oryza sativa
 <220>
 <221> misc_feature
 <222> (560)...(650)
 <223> segment of the T-DNA insert in line 1B-207-27

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 tcccattgag agtgcaaaat ctcaactcaac ttactgcatt gcttctccag aataactctc 180
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 <212> DNA
 <213> Oryza sativa
 <220>
 <221> misc_feature
 <222> (1311)...(1400)
 <223> segment of the T-DNA insert in line 1B-138-07

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 ggcctccgcc ggctcccat ggccgcgccg ctctccaccg ccgccgccgc ctctggtctc 180
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<210> 6

<211> 232

<212> DNA

<213> Oryza sativa

<220>

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<222> (1)...(101)

<223> segment of the T-DNA insert in line 1D-059-12

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aggattcgtc	tcctctcctt	tttgttcatt	atcctgtctg	tgtgtgattc	tggaacttctg	180
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<210> 7

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<222> (148)...(246)

<223> segment of the T-DNA insert in line 1C-087-40

<400> 7

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agaacttttt tattcttatg aatgtcattt ttgtttcatg taagttctat taaaattact 120
accaattaat gtttgatgtt catttcattc aaacacggat ccgaggtacc aggtaccagg 180
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<210> 8

<211> 370

<212> DNA

<213> Oryza sativa

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<221> misc_feature

<222> (1)...(218)

<223> segment of the T-DNA insert in line 1C-017-14

<400> 8

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tatgtaaatt                                           370
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<210> 9

<211> 214

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (126)...(214)

<223> segment of the T-DNA insert in line 1C-038-56

<400> 9

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gttctgaaga tggacctgac ctgttggttg gtctcttcag agtttttagg agttgagaca 120
aagcctatcc gaggtaccag gtaccagggt agttccattc ttactaccac ggtgctattt 180
tttttgctat gtggctaatt acatgactaa cttg                                           214
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<210> 10

<211> 514

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (1)...(113)

<223> segment of the T-DNA insert in line 1C-041-47

<400> 10

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514

<210> 11

<211> 603

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (512)...(603)

<223> segment of the T-DNA insert in line 1C-064-20

<400> 11

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gttccattct tactaccacg gtgctatgtt ttttgctatg tggctaatta catgactaac 600
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<210> 12

<211> 401

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (1)...(96)

<223> segment of the T-DNA insert in line 1C-109-35

<400> 12

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ctatcgcaaa ggatccgtgt ccttatttat gacacacatg acacacctac accccttatc 300
attatatttg ttttttagatt tgtgcgtata atacagattt caatagagca taacattatg 360
atttttcttt tccgtacaac acacgaatct caataaaata t                                     401

```

<210> 13

<211> 628

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (528)...(628)

<223> segment of the T-DNA insert in line 1C-109-51

<400> 13

```

gtggcggaac acctttcctt cttggttcag aagatgagat ggatgccttc actggttgga 60
tcagtgtatga aacacttaaa tatactctga aatgtggtgt aggctacttg catgaagggt 120
taagtgtatct ggaacaggaa gttgtaactc agctgtttct cagtgggagg atccaagtgt 180
gtgttgcgag tagcactgtg tgctggggaa gatcattgcc tgcccatctg gtggttggtga 240
tggaaccca gtattatgat ggccgggaga atgctcatalc tgattatcca atcactgatc 300
tactccaaat gatgggtcat gctagcaggc ctcttcaaga taactcaggg aaatgtgtta 360
tattgtgtca tgccgctcgc aaggaatact acaagaagtt cctttttgag gccttccctg 420
ttgagagcca tcttcaccac ttcttgcagt atcatatgaa cgctgagggtg gtggttggtg 480

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```

tcatagaaaa caagcaagat gctgtggatt accttacttg gaccttcattg tcaaacacgg 540
atccgaggtta ccaggtacca ggtgagttcc attcttacta ccacggtgct attttttttg 600
ctatgtggct aattacatga ctaacttg                                     628

```

<210> 14
 <211> 377
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (1)...(61)
 <223> segment of the T-DNA insert in line 1C-056-07

```

<400> 14
acaagccgta agtgcaagtg ccaaaatttg tgaagaaaat tacttccttc atttcacaat 60
tttcttcagc attaacacag tgtactacat ggcacccttt gccaccatga tactggctct 120
accagcagtg ttacttgaag gaggcggtgt gggtacctgg ttctacacac atgactccat 180
tgcttctgca ctagtatatca tcataggctc tggagtgcct gcattttgcc taaacttctc 240
cattttctac gtgatccatt caaccactgc agtgaccttc aatgttgctg gcaacctgaa 300
agtagcaacc atttggccta tgctttgttc ttttcatata ttctgctcga tcattttcta 360
gaactgatca ttgcgct                                     377

```

<210> 15
 <211> 422
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (351)...(422)
 <223> segment of the T-DNA insert in line 1C-100-32

```

<400> 15
ctaaactgac cactcttata agttttatta ctttatactg tagatgtctt gctgtcctgt 60
aactcaatat gctaccact aatatctagg agttaccatt gtactaaaaa tgtataaaac 120
atggttgata ggagttcaga aagtgcattt atctgggtac atccgatcac tggtagaata 180
tgttaccact tgaaccaaac tttatgtaat ttataatggg atatttgcaa ctacggaatc 240
ttttactgct catgcaggat cacaaaggaa tttcaaatgc tgcaccagct gattgtccat 300
tgatcccact attggtgcc aagtagatc aatcagaagg tacagtggat accaggtgag 360
ttccattctt actaccacgg tgctatTTTT tttgctatgt ggctaattac atgactaact 420
tg                                     422

```

<210> 16
 <211> 335
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (259)...(335)
 <223> segment of the T-DNA insert in line 1C-142-27

```

<400> 16
taagtgaagtc catctgctat ctagctctag tttccttttg ttaaacactt tgaaaggact 60
ttggttcgat agcaaccgct gcagttgcaa atttgcaata ttgttttagc agtagcagcc 120
tgcaactgtcg ttgattgagg attcgttgct tgttttgcct accgtcatgg gcctttttca 180
ggtcaccgac cgcacgagg ataagagcca agattctgta cgcgacgtcg aagcaagggc 240
tgaggcgggg gcttgacgga ggtaccagg gagttccatt ctactacca cggtgctatt 300
ttttttgcta tgggtaaat tacatgacta acttg                                     335

```

<210> 17
 <211> 425

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (332)...(425)

<223> segment of the T-DNA insert in line 1C-140-04

<400> 17

```

gctttccagg tatatataca taaaatccat cgatcatgca tgtcagaagc tcatcatgct 60
cagatgctca tcctgctcac gctcaatgct catgctctgc tgaaatttgg cggaatttgt 120
tgcacgcatg ttgtgtttcc gtattgcatc atgtttgtat atgccaagat atgtgcttac 180
taccgtgtga gcaatgctgt tcaagaactg aatttgtttt tgcaaagtgt tcacacctgg 240
agtaggtgga aggggcagct gcagaggatg ggaggaagcc cagcatttgg gacaccttca 300
tccatcaagg tccaaaaaaa tggagtagat gacacggatc cgaggtacca ggtaccaggt 360
gagttccatt cttactacca cggtgctatt ttttttgcta tgtggctaata tacatgacta 420
acttg

```

<210> 18

<211> 1149

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-115-22 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (394)...(395)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-115-22

<400> 18

```

aagcttaata tattaggagt agtaagctag cgtgtgagga agattcataa ccatatatca 60
tcttaattag cctttgtgat ttagcttaat cacatggcta aggcacaacc acccatccac 120
ttaactcttc attactacgc tagctacacg aggagagtag ctagctagta caggccccgg 180
caagcataaa tagcagcgtc ccctgcttcc tttcttcacg gtcctcagct catcatctgc 240
atgcagttca ctggcacacca cacagcttag cttgctcagc ttcactgac ttcttagctg 300
cagctacttc actttgcata gtttgatcga actaaataac tcaccaagtt agctgtaatg 360
gccaaagtga tcctcgccac cttcgccgct gtgttcattg cgtcgcgcgc cacctccctc 420
gccggcgacc cggacatgct ccaggacgct tgcgtcgccg actacaagtc cctcaaaggc 480
cgtaagtgtt ggaccattat gtgtcatcga ttcataaaat atgaattgac ctattttttt 540
ttaacgaccc gtacaagaca gtgcgaagat tcatattaac gtatatatgt atgtcgtgca 600
gcgctgcggc tgaacgggtt cccgtgcaag aggatagaga acgtgacggc gaacgacttc 660
ttcttcgatg ggctgatgaa ggccgggaac acggggaaac cgggtggggtc ggtggtgacg 720
gcggcgagcg tggagagcct gccggggctg aacacgatgg ggggtgtccat ggcgcgatc 780
gactacgcgc catgggggct gaacccaccg cacacgcac cccgtgccac cgagatcatc 840
ttcgtcgtcg agggctccct cgacgtcggc ttcgtcacca ccgccaacaa gctcttcacc 900
cgacaccgtc gcaaggggga ggtgttcgtc ttcccgcggg ggctcgtcca cttccagaag 960
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cagtcacatg ccgcccgcgt cttcggcgcc gcgcccgcgc tgccgtcgga cacgctggcc 1080
agggcgttcc aggtcgacgg cggcatggct gagttcatca agtccaagtt cgtcccggcc 1140
aaatactag

```

<210> 19

<211> 2971

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-164-43 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (577)...(578)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-164-43

<400> 19

caaaaaggcg	cctctaagaa	ttcctcccaa	acttttttgg	gttggtcaagc	cgtgcgtttc	60
ggggtacatc	aacggcgccg	atgagctccc	ggatggcccg	atcggcgatc	ctccgtcacg	120
tcggcgccgt	ccgcctcttc	accgcgtcgg	cgacctctcc	ggcgccggcg	gcggcgccgg	180
cggcgagggc	gttccttgca	ggcggagaag	ccgtcccccg	ggtgtggggg	ttgcggctga	240
tgtccacgtc	gtccgtggcg	tcgacggagg	cggcggccaa	ggcggaggcc	aagaaggcgg	300
acgcggagaa	ggaggtgggt	gtcaacagct	actggggcat	cgagcagtcg	aagaagctgg	360
tgcgggagga	cggcacggag	tggaagtggg	cttgctttag	ggtagcttgc	cttcgctttg	420
ctcctgatcg	gtttcctgtt	tcgattctgt	ttgtcccgtg	gattgatcgc	cagatcgaag	480
tatccatact	ccgagatagt	aggctcggtc	cttaacttgt	cgcgccggcg	tgtgtaattt	540
tggtttgatt	ttctccgcag	ccatgggaga	cctacaccgc	ggacacttcg	atcgatctga	600
cgaagcacca	cgtgcccaag	acgctgctcg	acaagatcgc	ctactggacc	gtcaagtgcg	660
tgcgctttccc	cactgatatc	ttcttccagg	tataattgtg	cttactcgat	caccatgcac	720
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aaaataataa	attttatatg	cgctcttcgg	gtactattca	ctgtctgatt	ttattatttt	1140
tgtttctcta	gttatagatc	aaatttagtc	atgcatgttt	gtgtatagac	ttatatcatc	1200
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gccggcgccc	atggctagct	ccctccctgc	catggctagc	tcgccacggg	ctccggcgga	2940
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<210> 20

<211> 4566

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-192-40 - genomic DNA without T-DNA insert

<221> misc_feature
 <222> (2273)...(2274)
 <223> location in genomic DNA where T-DNA was inserted
 to create line 1B-192-40

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 caaactagtc atgttcaaca ggaatgcatt gactattcga ccaagaatat ggcaccatcc 180
 aacaatcaac atgggtaaaa gatgtataaa cgcctattaa tataaatgtc ctagtccact 240
 ataagaatca aaagcatcta aaaactgaaa ccatattgtc caaaatacac accagcaaag 300
 atggtatgtg cagctataca cattgcagtc gtagcaatgc tcgtctccct tacagcatta 360
 gcaatagctg acgaatccga caataaccaa cggaagctc tgctctgcat caaatcacac 420
 ctctcaagcc cagagggagg cgccctcacc acatggaaca atacctcgct cgacatgtgc 480
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 gacatggagg cacagggcct cagcggagaa atcccaccct gcatctccaa cctctcgtcc 600
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 cgccttggtg cgcttcgcaa cctttcgtcc ctggacttaa caaacaacaa cattcatggc 780
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gaagacaccc taccaatgaa atatttactg atggcttgac actccgcatg tatgtcaatg 3540
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agaagatcgg atctagctaa gacagtccca actaaaccaa tgcttccctg aacacgatga 4440
agttaagat agaattaaaa tatccagtaa gcaaataac caatctaact agagcaatcc 4500
aagagatcca aacgatgcgg tcttgaagaa tgccaataaa gccgatacaa ttgccaaggc 4566
ctacgg

```

<210> 21

<211> 1914

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (906)...(907)

<223> location in genomic DNA where T-DNA was inserted
to create line 1B-207-27

<400> 21

```

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ctgccacatg gcaggaagct caactggagc tctgcagccc cagtctgcac ttcatgggtt 180
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cttaggtcca atcgcatcac tgttgatctc cctcctgaag taggatccat tccttctctc 360
cattccctat atcttcagca taataaccta tccgggatca taccgacttc cttacttcc 420
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cctgacctcc aactcccaaa attgaggcat ttgaatttga gcaacaataa cctcagtggg 600
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<223> line 1B-138-07 - genomic DNA without T-DNA insert

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<223> location in genomic DNA where T-DNA was inserted
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<212> DNA

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to create line 1D-059-12

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<223> line 1C-087-40 - genomic DNA without T-DNA insert

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<223> location in genomic DNA where T-DNA was inserted
to create line 1C-087-40

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<223> line 1C-017-14 - genomic DNA without T-DNA insert

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<223> location in genomic DNA where T-DNA was inserted
to create line 1C-017-14

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<210> 26

<211> 2034

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-038-56 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (125)...(126)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-038-56

<400> 26

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2034

<210> 27

<211> 4284

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-041-47 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2471)...(2472)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-041-47

<400> 27

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<210> 28

<211> 3234

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-064-20 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2690)...(2691)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-064-20

<400> 28

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<210> 29

<211> 3677

<212> DNA

<213> *Oryza sativa*

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-35 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2301)...(2302)

<223> location in genomic DNA where T-DNA was inserted to create line 1C-109-35

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<211> 8093

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-51 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (6570)...(6571)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-109-51

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<211> 1383

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-056-07 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (516)...(517)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-056-07

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<210> 32

<211> 7726

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-100-32 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (5051)...(5052)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-100-32

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<210> 33

<211> 2417

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (2020)...(2021)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-142-27

<400> 33

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<210> 34

<211> 4941

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-140-04 - genomic DNA without T-DNA insert

<221> misc_feature

<222> (773)...(774)

<223> location in genomic DNA where T-DNA was inserted
to create line 1C-140-04

<400> 34

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accggttaca	aatcggtcac	t				4941

<210> 35

<211> 672

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 18-115-22 coding sequence

<400> 35

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atcgactacg	cgcatggggg	gctgaaccca	cgcacacgc	atccccgtgc	caccgagatc	360
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aagaacaacg	gcaacacgcc	ggcggttcgcc	atcgccgcct	tgaacagcca	gctccccggg	540
acgcagtcca	tcgccgccgc	gctcttcggc	gccgcgccgc	cgctgccgtc	ggacacgctg	600
gccaggcgct	tccaggtcga	cggcggcgatg	gtcgaagtca	tcaagtccaa	gttcgtcccc	660
cccaaatact	ag					672

<210> 36
 <211> 999
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-164-43 coding sequence

<400> 36						
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ggcggagaag	ccgtccccgg	ggtgtggggg	ttgcggctga	tgtccacgtc	gtccgtggcg	180
tcgacggagg	cggcgggcaa	ggcgagggcc	aagaaggcgg	acgcggagaa	ggaggtggtg	240
gtcaacagct	actggggcat	cgagcagtcg	aagaagctgg	tgcgggagga	cggcacggag	300
tggaagtggg	cttgctttag	gccatgggag	acctacaccg	cggacacttc	gatcgatctg	360
acgaagcacc	acgtgccccaa	gacgctgctc	gacaagatcg	cctactggac	cgtaagtcg	420
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gagacgggtg	cggcgggtgcc	ggggatgggtg	ggcggcatgc	tgctccacct	ccggtccctc	540
cggcgcttcg	agcagagcgg	cggctggatc	cgcacgctgc	tggaagaggc	cgagaacgag	600
cgcatgcacc	tgatgacctt	catggagggtg	gcgaacccaa	agtggtagca	gcgcgccctc	660
gtcatcaccg	tccagggcgt	cttcttcaac	gcctacttcc	tgggttacct	cctctcccc	720
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gacgaggtc	accaccgcga	cgtcaatcac	ttcgcaticg	acatccatta	ccagggcgatg	960
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<210> 37
 <211> 3216
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1B-192-40 coding sequence

<400> 37						
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ctctcaagcc	cagagggagg	cgccctcacc	acatggaaca	atacctcgct	cgacatgtgc	180
acctggcgcg	gcgtgacatg	ctccagcgag	ctcccaaagc	ctcgtttggt	cgtaggccttg	240
gacatggagg	cacagggcct	cagcggagaa	atccccaccct	gcatctccaa	cctctcgtcc	300
ctcacgagaa	tccacctccc	caacaatggc	ctctccggtg	gcctcgcatc	cgcagccgat	360
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cgccttggtg	cgcttcgcaa	cctttcgtcc	ctggacttaa	caaacaacaa	cattcatggc	480
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gccaaacaaca	atcttgaggg	gataatgcct	cctggtatag	gaaacactct	tcctaacatc	1020

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cgatgcaaac	tgggaggggt	ggaggggtatt	ctcacatgta	cgataagaga	aattgcatca	3180
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<210> 38

<211> 1914

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-207-27 coding sequence

<400> 38

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ctgccacatg	gcaggaagct	caactggagc	tctgcagccc	cagctcgac	ttcatgggtt	180
gggggtgact	gcacaccaga	caatagccgc	gtgcaaacac	tacgcctacc	agcagtaggg	240
ctctttggcc	cgctaccctc	agacacgctt	ggcaagcttg	atgccctgga	ggtattgagc	300
cttaggtcca	atcgcatcac	tgttgatctc	cctctgaag	taggatccat	tccttctctc	360
cattccctat	atcttcagca	taataacct	tccgggatca	taccgacttc	ccttacttcc	420
actttaacat	ttctagatct	gtcatataac	acttttgatg	gagaaatccc	attgagagt	480
caaaatctca	ctcaacttac	tgcatgtgct	ctccagaata	actctctttc	tggaacctc	540
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ccaataccac	cttccttgca	aagattccca	gccaatctct	tcttggggaa	tgcttttcta	660
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caacggccaa	aaatggacga	ggtgatcagg	aggatcggtg	agatccgga	ttcctactcc	1860
gggtcaagaa	caccaccgga	ggagaagcag	aaggatgaat	ctgcagcgcc	atga	1914

<210> 39

<211> 1571

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1B-138-07 coding sequence

<400> 39

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gataaactgg	cagagaacat	tacaaccgaa	caggggaaga	caactgaagga	tgcttggggc	360
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tgaatatgta	tcaaatgttt	ctaacgggat	tgacaccttt	agcattaggg	agccacttgg	480
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cggtcacgca	gcagtggaa	gagtcgccgg	ctcagcgcgt	ctccctctcc	atgccaccct	1560
cgagaagtga	a					1571

<210> 40

<211> 1323

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1D-059-12 coding sequence

<400> 40
 atggccgccc ccgccaccgc cgccgtcccc ctcgacgagg ccaaagccaa ggaggttctc 60
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 acagtcgagg agagcgagga tggcgtgagc ttggcactca tctgctcctt ctcgcggatg 180
 aagaagcacc taggcctgga cgcggacgtg aagcaggaga ccatgccgga ggagacggtg 240
 ctcgccgttg ctgagggtgct gcggcggttc tcggccctcc gtgtcaccga ggataagaaa 300
 gttggtagat caattgagtt gtcgaaactg gatgagatca tggagcaagt ggactctagg 360
 acaattgctg catcaccatt tccttacaat gtaaagctgg aagatgttca gtctttcttt 420
 gctcagtatg gcaagggtgaa cagtgtgagg ctacctcgac atattgccga caaacgacac 480
 ttctgtggca ctgcttttagt cgaattttca gaagaagagg aagcaaatgc tgtattaaag 540
 aatactcttg tttttgcagg agcagatctg gaaataaaac caaagaatt cgatactgaa 600
 agagaggcta agaaagaagc ttatgagaag tcacaaccta ctaagaatgg tcatgatgag 660
 tatccaaaag gtctaattgt ggccttcaag ctgaagataa ttcaaattga tgggtggcatg 720
 gcagaaaatg gtggggacaa agaggggtgaa actgatgatg ccaataaatc aagaacaggg 780
 catgacgaga aaatccctga gaacagtgat atcaaggaag acttgtcaga tgatgttgag 840
 aagtcaaaag aggcagctgc tcaatctggt aagaaaggag aaagtccttc agaaaatgcg 900
 gatgatccaa tttcaaggga agattttaaa gaagaatttg gcaaattcgg cacagtgcgg 960
 tatgtggact tcagcatagg ggaggattca ggatacattc gggtcgagga ttctaaggca 1020
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 cataatgcac cttaggaggt gggctgaaac ttaaaataga agttgaagcc 1260
 ttatggcaca caagaatgcc aacacatata tttggagtta tattatcatg gaactggcag 1320
 taa 1323

<210> 41
 <211> 2568
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-087-40 coding sequence

<400> 41
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 tctctctggg cgcgccctca ggactccatc tcgcgccact ctttcgacac gccgctctac 120
 cggttcaacg tccccgatct ccgcgtcggc acgctcgact ccctcctcgc cctcagcgac 180
 gatctcgta agtccaacgt cttcatcgag ggggtctcgc acaagatccg gaggcagatc 240
 gaggagctag agcgcgccgg ggggtgtcga agtggggctc tcaccgttga cggcgtcccc 300
 gtcgacacct acctcacctt tgtgtgggat gagggcaaat acccaacgat gtcaccgctc 360
 aaggagattg tcggcagcat ccaatcacag gtctccaaga ttgaagatga catgaagggt 420
 cgaggagcgg aatacaataa tgtaaggagc cagcttagtg cgatcaacag aaagcaaact 480
 ggattagcag ttcgtgatct ttccaatctg gtaaaaccag aggatattgg cacatcagaa 540
 catctagtga cactccttgc agttgttcct aagtactctc aaaaggattg gttgtcaagc 600
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 gagtatgctc tctacacggt aacattgttt gctaagggtg ttgacaactt taagggtccg 720
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 caatgtgtgt atgccagcta accatttatg tacgtcatgc taaagtgcga 900
 aactttgtgc ttctctatgt attcagttcc tggatgcact tctgtgctgt gcgtgtcttt 960
 gtagagagca ttcttagata tggctctccc ccatcattcc tgtctgctgt tctagcacct 1020
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 atttactgga aatctgaaga cgatgttggt gtagctgggtc tgggacaccg tgtaagatgt 1140
 tgtggatatt atgtttttgt aactttgagc agccagaagg acaagttggg ggttatgtat 1200
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 gaggagatga tgggtcaagg gaaggagata cacgtgatgt ccaaccggcg tcgcaagcgc 1320

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gaggaggacg	acaccgtgct	tgtgcagtcg	gagtcgcgca	acaaggtgag	ggacgacatc	2520
gcgcacaacc	tcctccaccg	cggattggcc	ggcaccgcct	tcttctga		2568

<210> 42

<211> 1413

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-017-14 coding sequence

<400> 42

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ctagtgtggt	ccaagctcac	cggaagagg	ctccgcctcc	cgccggcccc	cgccggcgcg	120
cccacgtcgc	gcaactggct	ccaggctcgg	gacgacctca	accaccgcaa	cctgatggcg	180
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gtgtacggcg	accactggcg	caagatgcgg	cggatcatga	cggtgccctt	cttcaccaac	420
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gagtacaact	acggtgactt	catccccgtc	ctccgcccct	tcctccgccc	ctacctcgca	720
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aagcgggtgg	tgcgccccga	cgagtttagg	ccggagagggt	tcctggagga	ggagaaggcc	1260
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cccggtatca	tcctcgcgct	gcccattcat	gggatcacgc	tcggccgcct	cgtccagagc	1380
ttcgacctgc	tgccgcggcc	cgggatggac	aag			1413

<210> 43

<211> 1227

<212> DNA

<213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-038-56 coding sequence

<400> 43
 gatgttcagc agcatagtgg cagtagcagc agctcaaccg aatccgacgt ccaagaaacc 60
 gccgctgtcg ccgtcgccga cccctccccg cggtcggagg tcgtcgacgg cgagagcccc 120
 ccgcagccgg gcggcgaggc ggcgagccat cagcagcagc agaaggagat gaagctgaag 180
 aagccggaca agatcctgcc atgcccgcgg tgcagcagca tggacaccaa gttctgtctac 240
 ttcaacaact acaacgtcaa ccagcctcgc cacttctgca agcactgcca gcgctactgg 300
 accgccggcg gcgccatgcg caacgtcccc gtcggcgccg gccgccgcaa gaacaagaac 360
 gccaccgccg ccgcccactt cctccaccgc gtccgcgcct gcgccgccgc cgccgccatg 420
 cccgcggcgc cccacgacgc caccaacgcc accgtgtctc gcttcggcgg cggcggaggc 480
 ggacacgacg cgctgcccgt caccctggac ctcgccgaca agatgacgcg cctcggcaag 540
 gaggggctcg tcgcccattg ccggaacgcc gacgccgccg ccgcgtgcag cgagggtgtcg 600
 agcaacaggg acgacgagca gatcggaac actgtagcaa aacctgcaaa cggtgtgcag 660
 cagcatcctc ctcctcctca tcatcatcat cattcagcca tgaacggtgg cggcatctgg 720
 ccctactaca cctcggggat cgcatcccg atatacccg cgccgccggc gtactggggc 780
 tgcattgatt cacctcttgg agcttggagc ctcccatggc cggccacagt ccagtctcag 840
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 ggcaagcatc ctagagaggg tggatgatc gatgcaagag atcaccatgg caatggtaaa 960
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 aaacatccgg cgatcacgag cttgccgctc ttgcacacca accccgtcgc gcttaccgga 1200
 tccgcgacct tccaggaggg atcttga 1227

<210> 44
 <211> 861
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-041-47 coding sequence

<400> 44
 atgggcatca agggtttgac gaagcttttg gcggaacaat cgcccaaggc gatgaaggag 60
 cagaagttcg agagctactt cggccggcgc attgccgtcg acgccagcat gagcatctac 120
 cagttcctct catttgcata ctgcaagagg gaggatgcca ccaaagaact aacagaggca 180
 gtagaggaag gagataaaga cgcaattgaa aaattcagca agagaactgt gaaggtcacg 240
 aagcagcaca atgaagaatg taaacgacta ttaagactta tgggggttcc tgttgtagag 300
 gtttatgcag ttgcatcaga agatatggac tctcttactt ttggagctcc acggtttctt 360
 cgtcatttga tggatccaag ttccaagaaa attccagtta tggaaattga agtcgcgaaa 420
 gttttggagg agcttgaact cactatggac caattcattg acttgtgcat cctatctgga 480
 tgtgactatt gtgatagcat taaaattgga ggtcaaacag ctctgaaact tattcgtcaa 540
 catgggtcca tagaaagcat tctggaaaac ataaataaag actatcagat tcctgaggac 600
 tggccttatc aagaagctcg acgcttgctc aaggaacca atgttacatt ggatattcct 660
 gagctgaaat ggaatgctcc cgatgaggaa gccatagaga agattaaatt tgccaagaac 720
 aaatcttccc aaggactcga atccttcttc aagccagttg ttagcacatc agtgcctctg 780
 aaaagaaagg acacttcaga aaaaccaacc aaagcagtcg ctaacaagaa aacaaaggga 840
 gccggcggaa agaagaata a 861

<210> 45
 <211> 1653
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)

<223> line 1C-064-20 coding sequence

<400> 45

atggcgtcgg	cccccggcga	cggcaagcag	ggcggcgggc	gcggcgggcc	ggcgggtggc	60
atcgacctcg	gaacgacctg	ctcgtgcgtg	gcgggtgtgg	ggcacgaccg	cgcgagggtc	120
atcgccaacg	accagcgcaa	ccgcctcacg	ccctcctgcg	tcgccttcac	cgccgacgac	180
gacgacagct	tcgtcggcga	cgccgccttc	aaccagtcgg	cactcaaccc	aaccaatacc	240
atctttgtga	agcgactgat	tggccgcgga	ttcagcgatg	attctgtaca	aaaagatatc	300
aagctttggc	ctttcaaagt	cgtggcaggt	caagaggaca	ggccgatgat	cgtgggtgagg	360
catgaaggcg	aggaaaggca	gttcatgccc	gaggagatct	cctccatggg	gctcgccaag	420
atgagggaga	cggccgaggt	gtacctcggc	aagacgggtca	cgaaggccgt	catcactgtc	480
ccggtctact	tcaacaacgc	gcagcggcag	gccaccatgg	acgccggcgc	catcgccggc	540
ctcaacgtga	tgcgcatcat	caacgagccc	accgccgccc	ccctcgccta	ctgtctcgag	600
aagatgcccc	tcagcaacaa	ggggaggatg	gtgctcgtgt	tcgatctcgg	tggcggcaca	660
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agagcgaaga	ggatgctgtc	atccacgatg	cagaccacca	ttgaggtaga	ctcgctccat	900
caaggcatcg	acttccgcgt	caccctcacc	cgatccccgat	ttgaggagct	gaacaaggat	960
ctcttcagca	agtgcattga	ggctatggag	aattgcctcc	gcgacgcca	ggtggacaag	1020
tggagtgttg	acgatgtcgt	cctcgtgggt	ggctccacc	gcatacccaa	ggtgcagaag	1080
atgctgagtg	agttcttcga	cgggaaggag	ctctgccgca	gcatacaacc	cgatgaagcc	1140
gtcgcgtatg	gcgccgccat	ccaggcctcc	atcttatgtg	gtggaaccga	tgataagagg	1200
ttggttgata	tgcttctccg	cgaagtcacg	ccgctctcgc	taggtgttga	gactgaagat	1260
aattgtacaa	tgagcgtggg	gatcccaagg	aacactgcaa	tcccgacca	gaagggtgaa	1320
aacttcacta	ctctctacga	caaccagatc	aacgtgagct	ttccggtgta	cgagggtgag	1380
agcgcaaaca	ccaaggacaa	caacctgctc	ggcgagttca	cgctatatgg	catccccccg	1440
gcaccaaga	gagtgccatc	tatcgatgtc	actttcgaca	ttgatgccaa	cggggtcttg	1500
aacgtttctg	ccgagcaca	ggtcaccgga	cagaagaaca	gcatacccat	cactaaccgc	1560
agcggacggc	tgaaccagga	ggaaatcgat	cgcattggctc	tggagcccga	gaggcacaag	1620
atgaagcgga	tcaagcttca	cgaagtagtc	taa			1653

<210> 46

<211> 1437

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-35 coding sequence

<400> 46

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gcggactggc	tgaacaaggg	ggacaacgcg	tggcagctgg	tggcgcgac	gctgggtggg	120
ctgcagagcg	tgccgggctt	ggtggtgctg	tacggcgggc	tgggtgaaga	gaagtgggcg	180
gtgaactcgg	cgttcatggc	gctctacgcc	ttcgccggcg	tgtggatctg	ctgggtcacc	240
tgggcgtaca	acatgtcgtt	cggggagaag	ctcctcccga	tctgggggaa	ggcgcgggcg	300
gcgctggacc	agggcctcct	cgtcggccgc	gccgcgctgc	cggcgacggg	ccactaccgc	360
gccgacggca	gcgtggagac	ggcggcggtg	gagccgctgt	acccgatggc	gacgggtggg	420
tacttccagt	gcgtgttcgc	cgccatcacc	ctcatcctcg	tcgccggctc	cctcctcggc	480
cgcatgagct	tcctcgccctg	gatgatcttc	gtcccgtctt	ggctcacctt	ctcctacacc	540
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tgccggcggt	acgtcatcca	cgtctccgcc	ggcatcgccg	gcttcaccgc	cgcttactgg	660
gtggggccaa	ggcgcgagaa	ggacagggag	aggttcccgc	cgaacaatat	actgttcacg	720
ctgacggggg	cagggtcgtg	gtggatgggt	tgggcagggg	tcaacggcgg	cggtccgtac	780
gccccaact	ccgtcgccctc	tatggccgtc	ctcaacacca	acatctgcac	cgccatgagc	840
ctcatcgtct	ggacatgcct	cgacgtcatc	ttcttcaaga	agccctccgt	cgtcggcgcc	900
gtccagggca	tgatcaccgg	cctcgtttgc	atcacccccc	ctgcagtggg	gcaggggtgg	960
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<210> 47

<211> 6534

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-109-51 coding sequence

<400> 47

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gccaaactcca	gcctcgtcct	caccaccgac	tcgcgcccc	gcgacacca	cgagcccacc	120
ggcgagcccc	agacgctctg	gggcaggatc	gaccccagga	gcttcggcga	ccgcgccgtc	180
caggccaagc	ccccgagct	cgaggagaag	ctcaccaagt	cccgaagaa	gaaggccgcc	240
gcctctgacc	ccgacgacct	ccaccgccgc	gacgccaagc	gcaggcgccg	cgccgcagcc	300
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aaggagacgc	gcgccccta	cgaggccctg	ctcagcgtca	tccagcaaca	gttcggcgga	420
cagccgctcg	acgtcctcgg	cggcgctgcc	gacgagggtg	tcgccgtcct	caagaatgac	480
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cagatgttcg	accagatcgt	ctccataggg	aagctcatca	cggatttcca	tgatgcctcg	600
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<210> 48
 <211> 543
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-056-07 coding sequence

<400> 48
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 aattcgccga gaagtcggat ggagatgctc cccctttag gcgacaagca agaaaaggtt 540
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<210> 49
 <211> 2436
 <212> DNA
 <213> Oryza sativa

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> line 1C-100-32 coding sequence

<400> 49
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<210> 50

<211> 429

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-142-27 coding sequence

<400> 50

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<210> 51

<211> 1344

<212> DNA

<213> Oryza sativa

<220>

<221> misc_feature

<222> (0)...(0)

<223> line 1C-140-04 coding sequence

<400> 51

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<210> 52
<211> 223
<212> PRT
<213> Oryza sativa

<220>
<221> PEPTIDE
<222> (0)...(0)
<223> line 1B-115-22 polypeptide sequence

<400> 52
Met Ala Lys Leu Ile Leu Ala Thr Phe Ala Val Val Phe Met Ala Leu
1 5 10 15
Ala Ala Thr Ser Leu Ala Gly Asp Pro Asp Met Leu Gln Asp Val Cys
20 25 30
Val Ala Asp Tyr Lys Ser Leu Lys Gly Pro Leu Arg Leu Asn Gly Phe
35 40 45
Pro Cys Lys Arg Ile Glu Asn Val Thr Ala Asn Asp Phe Phe Phe Asp
50 55 60
Gly Leu Met Lys Ala Gly Asn Thr Gly Asn Ala Val Gly Ser Val Val
65 70 75 80
Thr Ala Ala Ser Val Glu Ser Leu Pro Gly Leu Asn Thr Met Gly Val
85 90 95
Ser Met Ala Arg Ile Asp Tyr Ala Pro Trp Gly Leu Asn Pro Pro His
100 105 110
Thr His Pro Arg Ala Thr Glu Ile Ile Phe Val Val Glu Gly Ser Leu
115 120 125
Asp Val Gly Phe Val Thr Thr Ala Asn Lys Leu Phe Thr Arg Thr Val
130 135 140
Cys Lys Gly Glu Val Phe Val Phe Pro Arg Gly Leu Val His Phe Gln
145 150 155 160
Lys Asn Asn Gly Asn Thr Pro Ala Phe Ala Ile Ala Ala Leu Asn Ser
165 170 175
Gln Leu Pro Gly Thr Gln Ser Ile Ala Ala Ala Leu Phe Gly Ala Ala
180 185 190
Pro Pro Leu Pro Ser Asp Thr Leu Ala Arg Ala Phe Gln Val Asp Gly
195 200 205
Gly Met Val Glu Phe Ile Lys Ser Lys Phe Val Pro Pro Lys Tyr
210 215 220

<210> 53
<211> 332
<212> PRT
<213> Oryza sativa

<220>
<221> PEPTIDE
<222> (0)...(0)
<223> line 1B-164-43 polypeptide sequence

<400> 53
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Val Arg Leu Phe Thr Ala Ser Ala Thr Ser Pro Ala Ala Ala Ala Ala
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Ala Ala Ala Arg Pro Phe Leu Ala Gly Gly Glu Ala Val Pro Gly Val
35 40 45
Trp Gly Leu Arg Leu Met Ser Thr Ser Ser Val Ala Ser Thr Glu Ala

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	Thr	Ala	Asp	Thr	Ser	Ile	Asp	Leu	Thr	Lys	His	His	Val	Pro	Lys	Thr
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	Leu	Arg	Ser	Leu	Arg	Arg	Phe	Glu	Gln	Ser	Gly	Gly	Trp	Ile	Arg	Thr
	Leu	Leu	Glu	Glu	Ala	Glu	Asn	Glu	Arg	Met	His	Leu	Met	Thr	Phe	Met
	Glu	Val	Ala	Asn	Pro	Lys	Trp	Tyr	Glu	Arg	Ala	Leu	Val	Ile	Thr	Val
	Gln	Gly	Val	Phe	Phe	Asn	Ala	Tyr	Phe	Leu	Gly	Tyr	Leu	Leu	Ser	Pro
	Lys	Phe	Ala	His	Arg	Val	Val	Gly	Tyr	Leu	Glu	Glu	Glu	Ala	Ile	His
	Ser	Tyr	Thr	Glu	Phe	Leu	Lys	Asp	Leu	Glu	Ala	Gly	Lys	Ile	Asp	Asn
	Val	Pro	Ala	Pro	Ala	Ile	Ala	Ile	Asp	Tyr	Trp	Arg	Leu	Pro	Ala	Asn
	Ala	Thr	Leu	Lys	Asp	Val	Val	Thr	Val	Val	Arg	Ala	Asp	Glu	Ala	His
	His	Arg	Asp	Val	Asn	His	Phe	Ala	Ser	Asp	Ile	His	Tyr	Gln	Gly	Met
	Glu	Leu	Lys	Gln	Thr	Pro	Ala	Pro	Ile	Gly	Tyr	His				

<210> 54
 <211> 1073
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1B-192-40 polypeptide sequence

<400> 54	Met	Val	Cys	Ala	Ala	Ile	His	Ile	Ala	Val	Val	Ala	Met	Leu	Val	Ser
1	Leu	Thr	Ala	Leu	Ala	Ile	Ala	Asp	Glu	Ser	Asp	Asn	Asn	Gln	Arg	Glu
	Ala	Leu	Leu	Cys	Ile	Lys	Ser	His	Leu	Ser	Ser	Pro	Glu	Gly	Gly	Ala
	Leu	Thr	Thr	Trp	Asn	Asn	Thr	Ser	Leu	Asp	Met	Cys	Thr	Trp	Arg	Gly
	Val	Thr	Cys	Ser	Ser	Glu	Leu	Pro	Lys	Pro	Arg	Leu	Val	Val	Ala	Leu
	Asp	Met	Glu	Ala	Gln	Gly	Leu	Ser	Gly	Glu	Ile	Pro	Pro	Cys	Ile	Ser
	Asn	Leu	Ser	Ser	Leu	Thr	Arg	Ile	His	Leu	Pro	Asn	Asn	Gly	Leu	Ser
	Gly	Gly	Leu	Ala	Ser	Ala	Ala	Asp	Val	Ala	Gly	Leu	Arg	Tyr	Leu	Asn

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Leu	Ser	115	Phe	Asn	Ala	Ile	Gly	120	Gly	Ala	Ile	Pro	Lys	125	Arg	Leu	Gly	Thr
130	Arg	Asn	Leu	Ser	Ser	135	Leu	Asp	Leu	Thr	Asn	Asn	Asn	Ile	His	Gly		
145	Ile	Pro	Pro	Leu	Leu	150	Gly	Ser	Ser	Ser	155	Ala	Leu	Glu	Ser	Val	Gly	
				165	Tyr	Leu	Thr	Gly	Gly	170	Ile	Pro	Leu	Phe	Leu	Ala	Asn	
				180	Arg	Tyr	Leu	Ser	185	Lys	Asn	Asn	Ser	190	Leu	Tyr	Gly	
				195	Ala	Ala	Leu	Phe	200	Asn	Ser	Ser	Thr	Ile	Arg	Glu	Ile	
				210	Glu	Asn	Asn	Leu	215	Ser	Gly	Ala	Ile	Pro	Val	Thr	Ile	
				225	Gln	Ile	Thr	230	Asn	Leu	Asp	Leu	Thr	235	Asn	Ser	Leu	
					245	Ser	Leu	Gly	Asn	Leu	Ser	Ser	Leu	Thr	250	Ala	Leu	
					260	Pro	Pro	Ser	Leu	Gly	Asn	Leu	Ser	Ser	Leu	Thr	Ala	
					275	Glu	Asn	Gln	Leu	Gln	Gly	Ser	Ile	Pro	Asp	Phe	Ser	
						290	Ala	Leu	Arg	Tyr	Leu	Asp	295	Leu	Ser	Tyr	Asn	
						305	Val	Asn	Pro	Ser	Val	Tyr	310	Asn	Met	Ser	Ser	
							Ala	Asn	Asn	Asn	Leu	Glu	315	Gly	Ile	Met	Pro	
								325	Gln	Val	Leu	Ile	330	Met	Ser	Asp	Asn	
								340	Ile	Gln	Val	Leu	345	Met	Ser	Asp	Asn	
									355	Pro	Lys	Ser	Leu	Ala	Asn	Ala	Ser	
									370	Ala	Asn	Asn	Ser	Leu	Arg	Gly	Val	
										385	Thr	Asp	Leu	Arg	Val	Val	Met	
											390	Val	Met	Leu	Tyr	Ser	Asn	
												395	Asn	Gln	Leu	Glu	Ala	
													410	Cys	Ser	Asn	Leu	
														415	Gln	Lys		
															430	Ser	Val	
																445	Ser	
																	460	
																	475	
																	490	
																	505	
																	520	
																	535	
																	550	
																	565	
																	580	
																	595	
																	610	

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Gln Ser Leu Ala Asn Leu Arg Gly Thr Lys Val Leu Asp Phe Ser Gln
 625 630 635 640
 Asn Asn Leu Ser Gly Ala Ile Pro Asp Phe Gly Thr Phe Thr Ser
 645 650 655
 Leu Gln Tyr Leu Asn Met Ser Tyr Asn Asn Phe Glu Gly Pro Ile Pro
 660 665 670
 Val Asp Gly Ile Phe Ala Asp Arg Asn Lys Val Phe Val Gln Gly Asn
 675 680 685
 Pro His Leu Cys Thr Asn Val Pro Met Asp Glu Leu Thr Val Cys Ser
 690 695 700
 Ala Ser Ala Ser Lys Arg Lys Asn Lys Leu Ile Ile Pro Met Leu Ala
 705 710 715 720
 Ala Phe Ser Ser Ile Ile Leu Leu Ser Ser Ile Leu Gly Leu Tyr Phe
 725 730 735
 Leu Ile Val Asn Val Phe Leu Lys Arg Lys Trp Lys Ser Asn Glu His
 740 745 750
 Met Asp His Thr Tyr Met Glu Leu Lys Thr Leu Thr Tyr Ser Asp Val
 755 760 765
 Ser Lys Ala Thr Asn Asn Phe Ser Ala Ala Asn Ile Val Gly Ser Gly
 770 775 780
 His Phe Gly Thr Val Tyr Arg Gly Ile Leu His Thr Glu Asp Thr Met
 785 790 795 800
 Val Ala Val Lys Val Phe Lys Leu Asp Gln Cys Gly Ala Leu Asp Ser
 805 810 815
 Phe Met Ala Glu Cys Lys Ala Leu Lys Asn Ile Arg His Arg Asn Leu
 820 825 830
 Val Lys Val Ile Thr Ala Cys Ser Thr Tyr Asp Pro Met Gly Ser Glu
 835 840 845
 Phe Lys Ala Leu Val Phe Glu Tyr Met Ala Asn Gly Ser Leu Glu Ser
 850 855 860
 Arg Leu His Thr Lys Phe Asp Arg Cys Gly Asp Leu Ser Leu Gly Glu
 865 870 875 880
 Arg Ile Ser Ile Ala Phe Asp Ile Ala Ser Ala Leu Glu Tyr Leu His
 885 890 895
 Asn Gln Cys Ile Pro Pro Val Val His Cys Asp Leu Lys Pro Ser Asn
 900 905 910
 Val Leu Phe Asn Asn Asp Asp Val Ala Cys Val Cys Asp Phe Gly Leu
 915 920 925
 Ala Arg Ser Ile Arg Val Tyr Ser Ser Gly Thr Gln Ser Ile Ser Thr
 930 935 940
 Ser Met Ala Gly Pro Arg Gly Ser Ile Gly Tyr Ile Ala Pro Glu Tyr
 945 950 955 960
 Gly Met Gly Ser Gln Ile Ser Thr Glu Gly Asp Val Tyr Ser Tyr Gly
 965 970 975
 Ile Ile Leu Leu Glu Met Leu Thr Gly Arg His Pro Thr Asn Glu Ile
 980 985 990
 Phe Thr Asp Gly Leu Thr Leu Arg Met Tyr Val Asn Ala Ser Leu Ser
 995 1000 1005
 Gln Ile Lys Asp Ile Leu Asp Pro Arg Leu Ile Pro Glu Met Thr Glu
 1010 1015 1020
 Gln Pro Ser Asn His Thr Leu Gln Leu His Glu His Lys Lys Thr Val
 1025 1030 1035 1040
 Pro Ser Arg Cys Lys Leu Gly Gly Val Glu Gly Ile Leu Thr Cys Thr
 1045 1050 1055
 Ile Arg Glu Ile Ala Ser Lys Leu Gly Gly Leu Arg Leu Ser Met Leu
 1060 1065 1070
 Thr

<210> 55
 <211> 637
 <212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-207-27 polypeptide sequence

<400> 55

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Met Gln Asp His Ile Leu Thr Ala Phe Leu Val Val Ser Leu Leu Phe
 1      5      10      15
Ala Cys Ile Pro Pro Ala Lys Ser Ala Asp Leu Asn Ser Asp Lys Gln
 20      25      30
Ala Leu Leu Ala Phe Ala Ala Ser Leu Pro His Gly Arg Lys Leu Asn
 35      40      45
Trp Ser Ser Ala Ala Pro Val Cys Thr Ser Trp Val Gly Val Thr Cys
 50      55      60
Thr Pro Asp Asn Ser Arg Val Gln Thr Leu Arg Leu Pro Ala Val Gly
 65      70      75      80
Leu Phe Gly Pro Leu Pro Ser Asp Thr Leu Gly Lys Leu Asp Ala Leu
 85      90      95
Glu Val Leu Ser Leu Arg Ser Asn Arg Ile Thr Val Asp Leu Pro Pro
100      105      110
Glu Val Gly Ser Ile Pro Ser Leu His Ser Leu Tyr Leu Gln His Asn
115      120      125
Asn Leu Ser Gly Ile Ile Pro Thr Ser Leu Thr Ser Thr Leu Thr Phe
130      135      140
Leu Asp Leu Ser Tyr Asn Thr Phe Asp Gly Glu Ile Pro Leu Arg Val
145      150      155      160
Gln Asn Leu Thr Gln Leu Thr Ala Leu Leu Leu Gln Asn Asn Ser Leu
165      170      175
Ser Gly Pro Ile Pro Asp Leu Gln Leu Pro Lys Leu Arg His Leu Asn
180      185      190
Leu Ser Asn Asn Asn Leu Ser Gly Pro Ile Pro Pro Ser Leu Gln Arg
195      200      205
Phe Pro Ala Asn Ser Phe Leu Gly Asn Ala Phe Leu Cys Gly Phe Pro
210      215      220
Leu Gln Pro Cys Pro Gly Thr Ala Pro Ser Pro Ser Pro Ser Thr
225      230      235      240
Ser Pro Ser Pro Gly Lys Ala Lys Lys Gly Phe Trp Lys Arg Ile Arg
245      250      255
Thr Gly Val Ile Ile Ala Leu Ala Ala Ala Gly Gly Val Leu Leu Leu
260      265      270
Ile Leu Ile Val Leu Leu Leu Ile Cys Ile Phe Lys Arg Lys Lys Ser
275      280      285
Thr Glu Pro Thr Thr Ala Ser Ser Ser Lys Gly Lys Thr Val Ala Gly
290      295      300
Gly Arg Gly Glu Asn Pro Lys Glu Glu Tyr Ser Ser Gly Val Gln Glu
305      310      315      320
Ala Glu Arg Asn Lys Leu Val Phe Phe Glu Gly Cys Ser Tyr Asn Phe
325      330      335
Asp Leu Glu Asp Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly
340      345      350
Ser Tyr Gly Thr Thr Tyr Lys Ala Val Leu Glu Asp Gly Thr Thr Val
355      360      365
Val Val Lys Arg Leu Lys Glu Val Val Val Gly Lys Lys Asp Phe Glu
370      375      380
Gln Gln Met Glu Ile Val Gly Arg Val Gly Gln His Gln Asn Val Val
385      390      395      400
Pro Leu Arg Ala Tyr Tyr Tyr Ser Lys Asp Glu Lys Leu Leu Val Tyr
405      410      415
Asp Tyr Ile Pro Ser Gly Ser Leu Ala Val Val Leu His Gly Asn Lys
420      425      430
Ala Thr Gly Lys Ala Pro Leu Asp Trp Glu Thr Arg Val Lys Ile Ser

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435 440 445
 Leu Gly Val Ala Arg Gly Ile Ala His Leu His Ala Glu Gly Gly Gly
 450 455 460
 Lys Phe Ile His Gly Asn Leu Lys Ser Ser Asn Ile Leu Leu Ser Gln
 465 470 475 480
 Asn Leu Asp Gly Cys Val Ser Glu Phe Gly Leu Ala Gln Leu Met Thr
 485 490 495
 Ile Pro Pro Ala Pro Ala Arg Leu Val Gly Tyr Arg Ala Pro Glu Val
 500 505 510
 Leu Glu Thr Lys Lys Pro Thr Gln Lys Ser Asp Val Tyr Ser Phe Gly
 515 520 525
 Val Leu Val Leu Glu Met Leu Thr Gly Lys Ala Pro Leu Arg Ser Pro
 530 535 540
 Gly Arg Glu Asp Ser Ile Glu His Leu Pro Arg Trp Val Gln Ser Val
 545 550 555 560
 Val Arg Glu Glu Trp Thr Ala Glu Val Phe Asp Val Asp Leu Leu Arg
 565 570 575
 His Pro Asn Ile Glu Asp Glu Met Val Gln Met Leu Gln Val Ala Met
 580 585 590
 Ala Cys Val Ala Ala Pro Pro Asp Gln Arg Pro Lys Met Asp Glu Val
 595 600 605
 Ile Arg Arg Ile Val Glu Ile Arg Asn Ser Tyr Ser Gly Ser Arg Thr
 610 615 620
 Pro Pro Glu Glu Lys Gln Lys Asp Glu Ser Ala Ala Pro
 625 630 635

<210> 56

<211> 523

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1B-138-07 polypeptide sequence

<400> 56

Met Ala Ala Pro Leu Ser Thr Ala Ala Ala Ala Ser Trp Leu Ser Asp
 1 5 10 15
 Ser Ala Ser Ser Pro Pro Arg Val Arg Leu Leu Ile Gly Gly Glu Phe
 20 25 30
 Val Glu Ser Arg Ala Asp Glu His Val Asp Val Thr Asn Pro Ala Thr
 35 40 45
 Gln Glu Val Val Ser Arg Ile Pro Leu Thr Thr Ala Asp Glu Phe Arg
 50 55 60
 Ala Ala Val Asp Ala Ala Arg Thr Ala Phe Pro Gly Trp Arg Asn Thr
 65 70 75 80
 Pro Val Thr Thr Arg Gln Arg Ile Met Leu Lys Tyr Gln Glu Leu Ile
 85 90 95
 Arg Ala Asn Met Asp Lys Leu Ala Glu Asn Ile Thr Thr Glu Gln Gly
 100 105 110
 Lys Thr Leu Lys Asp Ala Trp Gly Asp Val Phe Arg Gly Leu Glu Val
 115 120 125
 Val Glu His Ala Cys Gly Met Gly Thr Leu Gln Met Gly Glu Tyr Val
 130 135 140
 Ser Asn Val Ser Asn Gly Ile Asp Thr Phe Ser Ile Arg Glu Pro Leu
 145 150 155 160
 Gly Val Cys Ala Gly Ile Cys Pro Phe Asn Phe Pro Ala Met Ile Pro
 165 170 175
 Leu Trp Met Phe Pro Ile Ala Val Thr Cys Gly Asn Thr Phe Val Leu
 180 185 190
 Lys Pro Ser Glu Lys Asp Pro Gly Ala Ala Met Met Leu Ala Glu Leu

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Ala	Met	Glu	Ala	Gly	Leu	Pro	Lys	Gly	Val	Leu	Asn	Ile	Val	His	Gly
210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285
Thr	His	Asp	Val	Val	Asn	Asn	Ile	Cys	Asp	Asp	Glu	Asp	Ile	Lys	Ala
Val	Ser	Phe	Val	Gly	Ser	Asn	Ile	Ala	Gly	Met	His	Ile	Tyr	Ser	Arg
Ala	Ser	Ala	Lys	Gly	Lys	Arg	Val	Gln	Ser	Asn	Met	Gly	Ala	Lys	Asn
His	Ala	Ile	Ile	Leu	Pro	Asp	Ala	Asp	Arg	Asp	Ala	Thr	Leu	Asn	Ala
Leu	Ile	Ala	Ala	Gly	Phe	Gly	Ala	Ala	Gly	Gln	Arg	Cys	Met	Ala	Leu
Ser	Thr	Ala	Val	Phe	Val	Gly	Gly	Ser	Glu	Pro	Trp	Ile	Arg	Pro	Gly
Ile	Arg	Glu	Asp	Glu	Leu	Val	Lys	Arg	Ala	Ser	Ser	Leu	Val	Val	Asn
Ser	Gly	Met	Ala	Ser	Asp	Ala	Asp	Leu	Gly	Pro	Val	Ile	Ser	Lys	Gln
Ala	Lys	Glu	Arg	Ile	Cys	Lys	Leu	Ile	Gln	Ser	Gly	Ala	Asp	Asn	Gly
Ala	Arg	Val	Leu	Leu	Asp	Gly	Arg	Asp	Ile	Val	Val	Pro	Asn	Phe	Glu
Asn	Gly	Asn	Phe	Val	Gly	Pro	Thr	Leu	Leu	Ala	Asp	Val	Lys	Ser	Glu
Met	Glu	Cys	Tyr	Lys	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Leu	Leu	Met
Lys	Ala	Glu	Ser	Leu	Asp	Asp	Ala	Ile	Gln	Ile	Val	Asn	Arg	Asn	Lys
Tyr	Gly	Asn	Gly	Ala	Ser	Ile	Phe	Thr	Thr	Ser	Gly	Val	Ser	Ala	Arg
Lys	Phe	Gln	Thr	Asp	Ile	Glu	Ala	Gly	Gln	Val	Gly	Ile	Asn	Val	Pro
Ile	Pro	Val	Pro	Leu	Pro	Phe	Phe	Ser	Phe	Thr	Gly	Ser	Lys	Ala	Ser
Phe	Ala	Gly	Asp	Leu	Asn	Phe	Tyr	Gly	Lys	Ala	Gly	Val	Gln	Phe	Phe
Thr	Gln	Ile	Lys	Thr	Val	Thr	Gln	Gln	Trp	Lys	Glu	Ser	Pro	Ala	Gln
Arg	Val	Ser	Leu	Ser	Met	Pro	Thr	Ser	Gln	Lys					

<210> 57

<211> 446

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 10-059-12 polypeptide sequence

<400> 57

Met	Ala	Ala	Ala	Ala	Thr	Ala	Ala	Val	Pro	Leu	Asp	Glu	Ala	Lys	Ala
1				5				10						15	
Lys	Glu	Val	Leu	Arg	Gln	Val	Glu	Phe	Tyr	Phe	Ser	Asp	Ser	Asn	Leu
Pro	Arg	Asp	Asn	Phe	Leu	Arg	Lys	Thr	Val	Glu	Glu	Ser	Glu	Asp	Gly
Leu	Val	Ser	Leu	Ala	Leu	Ile	Cys	Ser	Phe	Ser	Arg	Met	Lys	Lys	His
Leu	Gly	Leu	Asp	Ala	Asp	Val	Lys	Gln	Glu	Thr	Met	Pro	Glu	Glu	Thr

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65	Val	Leu	Ala	Val	Ala	Glu	Val	Leu	Arg	Arg	Ser	Ser	Ala	Leu	Arg	Val
				85					90						95	
Thr	Glu	Asp	Gly	Lys	Lys	Val	Gly	Arg	Ser	Ile	Glu	Leu	Ser	Lys	Leu	
			100					105					110			
Asp	Glu	Ile	Met	Glu	Gln	Val	Asp	Ser	Arg	Thr	Ile	Ala	Ala	Ser	Pro	
		115					120					125				
Phe	Pro	Tyr	Asn	Val	Lys	Leu	Glu	Asp	Val	Gln	Ser	Phe	Phe	Ala	Gln	
	130					135					140					
Tyr	Gly	Lys	Val	Asn	Ser	Val	Arg	Leu	Pro	Arg	His	Ile	Ala	Asp	Lys	
	145			150						155					160	
Arg	His	Phe	Cys	Gly	Thr	Ala	Leu	Val	Glu	Phe	Ser	Glu	Glu	Glu	Glu	
			165						170					175		
Ala	Asn	Ala	Val	Leu	Lys	Asn	Thr	Leu	Val	Phe	Ala	Gly	Ala	Asp	Leu	
			180					185					190			
Glu	Ile	Lys	Pro	Lys	Lys	Glu	Phe	Asp	Thr	Glu	Arg	Glu	Ala	Lys	Lys	
		195					200					205				
Glu	Ala	Tyr	Glu	Lys	Ser	Gln	Pro	Thr	Lys	Asn	Gly	His	Asp	Glu	Gly	
	210					215					220					
Tyr	Pro	Lys	Gly	Leu	Ile	Val	Ala	Phe	Lys	Leu	Lys	Ile	Ile	Gln	Ile	
	225				230					235					240	
Asp	Gly	Gly	Met	Ala	Glu	Asn	Gly	Gly	Asp	Lys	Glu	Gly	Glu	Thr	Asp	
			245						250					255		
Asp	Ala	Asn	Lys	Ser	Arg	Thr	Gly	His	Asp	Glu	Lys	Ile	Pro	Glu	Asn	
		260						265					270			
Ser	Asp	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Asp	Val	Glu	Lys	Ser	Lys	Glu	
		275					280					285				
Ala	Ala	Ala	Gln	Ser	Val	Lys	Lys	Gly	Glu	Ser	Pro	Ser	Glu	Asn	Ala	
	290					295					300					
Asp	Asp	Pro	Ile	Ser	Arg	Glu	Asp	Phe	Lys	Glu	Glu	Phe	Gly	Lys	Phe	
	305				310					315					320	
Gly	Thr	Val	Arg	Tyr	Val	Asp	Phe	Ser	Ile	Gly	Glu	Asp	Ser	Gly	Tyr	
			325						330					335		
Ile	Arg	Phe	Glu	Asp	Ser	Lys	Ala	Ala	Glu	Lys	Ala	Arg	Ala	Leu	Ala	
			340				345						350			
Ala	Ile	Ser	Asp	Glu	Gly	Gly	Leu	Ile	Met	Lys	Gly	His	Leu	Val	Thr	
		355					360					365				
Leu	Glu	Pro	Val	Ser	Gly	Gln	Ala	Glu	Lys	Asp	Tyr	Trp	Ser	Ala	Ile	
	370					375					380					
Lys	Gly	Gly	Gln	Gly	Lys	Tyr	Arg	Asp	Asn	Arg	Ser	Asn	Arg	Gly	Arg	
	385				390					395					400	
Ala	Asp	Pro	Leu	Lys	Tyr	His	Asn	Ala	Pro	Arg	Met	Asn	Leu	Arg	Ser	
				405					410					415		
Gly	Leu	Lys	Leu	Lys	Ile	Glu	Val	Glu	Ala	Leu	Trp	His	Thr	Arg	Met	
			420					425					430			
Pro	Thr	His	Ile	Phe	Gly	Val	Ile	Leu	Ser	Trp	Asn	Trp	Gln			
		435					440					445				

<210> 58
 <211> 859
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-087-40 polypeptide sequence

<400> 58
 Met Ala Thr Arg Tyr Trp Ile Val Ser Leu Pro Val Gln Thr Pro Gly
 1 5 10 15
 Ser Thr Ala Asn Ser Leu Trp Ala Arg Leu Gln Asp Ser Ile Ser Arg

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			20					25				30			
His	Ser	Phe	Asp	Thr	Pro	Leu	Tyr	Arg	Phe	Asn	Val	Pro	Asp	Leu	Arg
		35					40					45			
Val	Gly	Thr	Leu	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Asp	Asp	Leu	Val	Lys
	50					55					60				
Ser	Asn	Val	Phe	Ile	Glu	Gly	Val	Ser	His	Lys	Ile	Arg	Arg	Gln	Ile
65					70					75				80	
Glu	Glu	Leu	Glu	Arg	Ala	Gly	Gly	Val	Glu	Ser	Gly	Ala	Leu	Thr	Val
			85						90					95	
Asp	Gly	Val	Pro	Val	Asp	Thr	Tyr	Leu	Thr	Arg	Phe	Val	Trp	Asp	Glu
			100					105					110		
Gly	Lys	Tyr	Pro	Thr	Met	Ser	Pro	Leu	Lys	Glu	Ile	Val	Gly	Ser	Ile
		115					120					125			
Gln	Ser	Gln	Val	Ser	Lys	Ile	Glu	Asp	Asp	Met	Lys	Val	Arg	Gly	Ala
	130					135					140				
Glu	Tyr	Asn	Asn	Val	Arg	Ser	Gln	Leu	Ser	Ala	Ile	Asn	Arg	Lys	Gln
145					150					155				160	
Thr	Gly	Ser	Leu	Ala	Val	Arg	Asp	Leu	Ser	Asn	Leu	Val	Lys	Pro	Glu
			165						170					175	
Asp	Met	Val	Thr	Ser	Glu	His	Leu	Val	Thr	Leu	Leu	Ala	Val	Val	Pro
			180					185					190		
Lys	Tyr	Ser	Gln	Lys	Asp	Trp	Leu	Ser	Ser	Tyr	Glu	Ser	Leu	Asp	Thr
		195					200					205			
Phe	Val	Val	Pro	Arg	Ser	Ser	Lys	Lys	Leu	Tyr	Glu	Asp	Asn	Glu	Tyr
	210					215					220				
Ala	Leu	Tyr	Thr	Val	Thr	Leu	Phe	Ala	Lys	Val	Val	Asp	Asn	Phe	Lys
225					230					235					240
Val	Arg	Ala	Arg	Glu	Lys	Gly	Phe	Gln	Val	Arg	Asp	Phe	Glu	Tyr	Ser
			245						250					255	
Ser	Glu	Ala	Gln	Glu	Ser	Arg	Lys	Glu	Glu	Leu	Glu	Lys	Leu	Met	Gln
			260					265					270		
Asp	Gln	Glu	Ala	Met	Arg	Ala	Ser	Leu	Leu	Gln	Trp	Cys	Tyr	Ala	Ser
		275					280					285			
Tyr	Ser	Glu	Asn	Thr	Ile	Tyr	Val	Arg	His	Ala	Lys	Val	Gln	Asn	Phe
	290					295					300				
Val	Leu	Leu	Tyr	Val	Phe	Ser	Ser	Trp	Met	His	Phe	Cys	Ala	Val	Arg
305					310					315					320
Val	Phe	Val	Glu	Ser	Ile	Leu	Arg	Tyr	Gly	Leu	Pro	Pro	Ser	Phe	Leu
			325						330					335	
Ser	Ala	Val	Leu	Ala	Pro	Ser	Gln	Lys	Gly	Glu	Lys	Lys	Val	Arg	Ser
			340					345					350		
Ile	Leu	Glu	Glu	Leu	Cys	Gly	Asn	Val	His	Ser	Ile	Tyr	Trp	Lys	Ser
		355					360					365			
Glu	Asp	Asp	Val	Gly	Val	Ala	Gly	Leu	Gly	Glu	His	Arg	Val	Arg	Cys
	370					375									

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Glu Ala Asp Phe Arg Arg Ala Phe Arg Met Ser Arg Pro Thr Phe His
 530 535 540
 Phe Leu Cys Asp Ala Leu Ala Ala Val Ala Lys Glu Asp Thr Ala
 545 550 555 560
 Leu Arg Ala Ala Ile Pro Val Arg Gln Arg Val Ala Val Cys Val Trp
 565 570 575
 Arg Leu Ala Thr Gly Glu Pro Leu Arg Val Val Ser Lys Arg Phe Gly
 580 585 590
 Leu Gly Ile Ser Thr Cys His Lys Leu Ile Leu Glu Val Cys Ala Ala
 595 600 605
 Ile Arg Asn Leu Leu Met Pro Arg Phe Leu His Trp Pro Asp His Pro
 610 615 620
 Thr Ser Thr Ala Tyr Lys Thr Arg Phe Glu Ala Thr Ser Gly Val Ser
 625 630 635 640
 Gly Val Val Gly Ala Met Tyr Thr Thr His Ile Pro Ile Ile Ala Pro
 645 650 655
 Lys Val Ser Val Ala Ala Tyr Leu Asn Arg Arg His Thr Glu Arg Asn
 660 665 670
 His Lys Thr Ser Tyr Ser Ile Thr Leu Gln Gly Val Val Gly Pro Asp
 675 680 685
 Gly Thr Phe Thr Asp Val Cys Ile Gly Trp Pro Gly Ser Met Ser Asp
 690 695 700
 Glu Gln Val Leu Arg Lys Ser Ala Leu His Gln Arg Ala Ser Ala Ala
 705 710 715 720
 Ala Gly Ser Met Ser Trp Val Val Gly Gly Ala Ser Tyr Pro Leu Thr
 725 730 735
 Glu Trp Met Leu Val Pro Tyr Ala Gln Arg Asn Leu Thr Trp Thr Gln
 740 745 750
 His Ala Phe Asn Glu Lys Val Gly Glu Val Arg Arg Val Ala Thr Glu
 755 760 765
 Ala Phe Val Arg Leu Lys Gly Arg Trp Ala Cys Leu Gln Lys Arg Thr
 770 775 780
 Glu Val Lys Leu Gln Asp Leu Pro Ala Val Leu Ala Ala Cys Cys Val
 785 790 795 800
 Leu His Asn Ile Cys Glu Thr Arg Gly Glu Asp Met Asp Pro Asp Leu
 805 810 815
 Arg Cys Asp Leu Pro Pro Asp Glu Glu Glu Asp Asp Thr Val Leu Val
 820 825 830
 Gln Ser Glu Ser Ala Asn Lys Val Arg Asp Asp Ile Ala His Asn Leu
 835 840 845
 Leu His Arg Gly Leu Ala Gly Thr Ala Phe Phe
 850 855

<210> 59

<211> 473

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-017-14 polypeptide sequence

<400> 59

Met Asp Ala Leu Leu Val Glu Lys Val Leu Leu Gly Leu Phe Val Ala
 1 5 10 15
 Ala Val Leu Ala Leu Val Val Ala Lys Leu Thr Gly Lys Arg Leu Arg
 20 25 30
 Leu Pro Pro Gly Pro Ala Gly Ala Pro Ile Val Gly Asn Trp Leu Gln
 35 40 45
 Val Gly Asp Asp Leu Asn His Arg Asn Leu Met Ala Leu Ala Arg Arg
 50 55 60

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Phe Gly Asp Ile Leu Leu Leu Arg Met Gly Val Arg Asn Leu Val Val
 65 70 75 80
 Val Ser Ser Pro Asp Leu Ala Lys Glu Val Leu His Thr Gln Gly Val
 85 90 95
 Glu Phe Gly Ser Arg Thr Arg Asn Val Val Phe Asp Ile Phe Thr Gly
 100 105 110
 Lys Gly Gln Asp Met Val Phe Thr Val Tyr Gly Asp His Trp Arg Lys
 115 120 125
 Met Arg Arg Ile Met Thr Val Pro Phe Phe Thr Asn Lys Val Val Ala
 130 135 140
 Gln Asn Arg Ala Gly Trp Glu Glu Glu Ala Arg Leu Val Val Glu Asp
 145 150 155 160
 Val Arg Arg Asp Pro Thr Ala Ala Thr Ser Gly Val Val Ile Arg Arg
 165 170 175
 Arg Leu Gln Leu Met Met Tyr Asn Asp Met Phe Arg Ile Met Phe Asp
 180 185 190
 Arg Arg Phe Asp Ser Val Asp Asp Pro Leu Phe Asn Lys Leu Lys Ala
 195 200 205
 Phe Asn Ala Glu Arg Ser Arg Leu Ser Gln Ser Phe Glu Tyr Asn Tyr
 210 215 220
 Gly Asp Phe Ile Pro Val Leu Arg Pro Phe Leu Arg Arg Tyr Leu Ala
 225 230 235 240
 Arg Cys His Gln Leu Lys Ser Gln Arg Met Lys Leu Phe Glu Asp His
 245 250 255
 Phe Val Gln Glu Arg Lys Arg Val Met Glu Gln Thr Gly Glu Ile Arg
 260 265 270
 Cys Ala Met Asp His Ile Leu Glu Ala Glu Arg Lys Gly Glu Ile Asn
 275 280 285
 His Asp Asn Val Leu Tyr Ile Val Glu Asn Ile Asn Val Ala Ala Ile
 290 295 300
 Glu Thr Thr Leu Trp Ser Ile Glu Trp Gly Ile Ala Glu Leu Val Asn
 305 310 315 320
 His Pro Ser Ile Gln Ser Lys Val Arg Glu Glu Met Ala Ser Val Leu
 325 330 335
 Gly Gly Ala Ala Val Thr Glu Pro Asp Leu Glu Arg Leu Pro Tyr Leu
 340 345 350
 Gln Ala Val Val Lys Glu Thr Leu Arg Leu Arg Met Ala Ile Pro Leu
 355 360 365
 Leu Val Pro His Met Asn Leu Ala Asp Gly Lys Leu Ala Gly Tyr Asp
 370 375 380
 Ile Pro Ala Glu Ser Lys Ile Leu Val Asn Ala Trp Phe Leu Ala Asn
 385 390 395 400
 Asp Pro Lys Arg Trp Val Arg Pro Asp Glu Phe Arg Pro Glu Arg Phe
 405 410 415
 Leu Glu Glu Glu Lys Ala Val Glu Ala His Gly Asn Asp Phe Arg Phe
 420 425 430
 Val Pro Phe Gly Val Gly Arg Arg Ser Cys Pro Gly Ile Ile Leu Ala
 435 440 445
 Leu Pro Ile Ile Gly Ile Thr Leu Gly Arg Leu Val Gln Ser Phe Asp
 450 455 460
 Leu Leu Pro Pro Pro Gly Met Asp Lys
 465 470

<210> 60
 <211> 408
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (O)...(O)
 <223> line 1C-038-56 polypeptide sequence

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<400> 60

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Asp Val Gln Gln His Ser Gly Ser Ser Ser Ser Thr Glu Ser Asp
1      5      10      15
Val Gln Glu Thr Ala Ala Val Ala Val Ala Asp Pro Ser Pro Arg Ser
20      25      30
Glu Val Val Asp Gly Glu Ser Pro Pro Gln Pro Gly Gly Glu Ala Ala
35      40      45
Ser His Gln Gln Gln Lys Glu Met Lys Leu Lys Lys Pro Asp Lys
50      55      60
Ile Leu Pro Cys Pro Arg Cys Ser Ser Met Asp Thr Lys Phe Cys Tyr
65      70      75      80
Phe Asn Asn Tyr Asn Val Asn Gln Pro Arg His Phe Cys Lys His Cys
85      90      95
Gln Arg Tyr Trp Thr Ala Gly Gly Ala Met Arg Asn Val Pro Val Gly
100     105     110
Ala Gly Arg Arg Lys Asn Lys Asn Ala Thr Ala Ala Ala His Phe Leu
115     120     125
His Arg Val Arg Ala Cys Ala Ala Ala Ala Met Pro Ala Ala Pro
130     135     140
His Asp Ala Thr Asn Ala Thr Val Leu Ser Phe Gly Gly Gly Gly Gly
145     150     155     160
Gly His Asp Ala Leu Pro Val Thr Leu Asp Leu Ala Asp Lys Met Thr
165     170     175
Arg Leu Gly Lys Glu Gly Leu Val Ala His Ala Arg Asn Ala Asp Ala
180     185     190
Ala Ala Ala Cys Ser Glu Val Ser Ser Asn Arg Asp Asp Glu Gln Ile
195     200     205
Gly Asn Thr Val Ala Lys Pro Ala Asn Gly Leu Gln Gln His Pro Pro
210     215     220
Pro Pro His His His His Ser Ala Met Asn Gly Gly Gly Ile Trp
225     230     235     240
Pro Tyr Tyr Thr Ser Gly Ile Ala Ile Pro Ile Tyr Pro Ala Ala Pro
245     250     255
Ala Tyr Trp Gly Cys Met Ile Pro Pro Pro Gly Ala Trp Ser Leu Pro
260     265     270
Trp Pro Ala Thr Val Gln Ser Gln Ala Ile Ser Ser Ser Ser Pro Pro
275     280     285
Thr Ser Ala Thr Pro Ser Val Ser Ser Phe Thr Leu Gly Lys His Pro
290     295     300
Arg Glu Gly Gly Asp His Glu Ala Arg Asp His His Gly Asn Gly Lys
305     310     315     320
Val Trp Val Pro Lys Thr Ile Arg Ile Asp Asn Ala Asp Glu Val Ala
325     330     335
Arg Ser Ser Ile Arg Ser Leu Phe Ala Phe Arg Gly Gly Asp Lys Val
340     345     350
Asp Asp Asn Asn Asp Asp Asp Gly Thr Ser Val His Lys Leu Ala Thr
355     360     365
Thr Val Phe Glu Pro Lys Arg Asp Gly Lys Thr Ala Lys His Pro Ala
370     375     380
Ile Thr Ser Leu Pro Leu Leu His Thr Asn Pro Val Ala Leu Thr Arg
385     390     395     400
Ser Ala Thr Phe Gln Glu Gly Ser
405

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<210> 61

<211> 290

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-041-47 polypeptide sequence

<400> 61

```

Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
 1      5      10      15
Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Arg Ile Ala
 20      25      30
Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ser Phe Ala Arg Tyr
 35      40      45
Ser Lys Arg Glu Asp Ala Thr Lys Glu Leu Thr Glu Ala Val Glu Glu
 50      55      60
Gly Asp Lys Asp Ala Ile Glu Lys Phe Ser Lys Arg Thr Val Lys Val
 65      70      75
Thr Lys Gln His Asn Glu Glu Cys Lys Arg Leu Leu Arg Leu Met Gly
 80      85      90
Val Pro Val Val Glu Val Tyr Ala Val Ala Ser Glu Asp Met Asp Ser
 100     105     110
Leu Thr Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser
 115     120     125
Ser Lys Lys Ile Pro Val Met Glu Phe Glu Val Ala Lys Val Leu Glu
 130     135     140
Glu Leu Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Ser
 145     150     155
Gly Cys Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala
 160     165     170
Leu Lys Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn
 175     180     185
Ile Asn Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu
 190     195     200
Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu
 205     210     215
Leu Lys Trp Asn Ala Pro Asp Glu Glu Ala Ile Glu Lys Ile Lys Phe
 220     225     230
Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro
 235     240     245
Val Val Ser Thr Ser Val Pro Leu Lys Arg Lys Asp Thr Ser Glu Lys
 250     255     260
Pro Thr Lys Ala Val Ala Asn Lys Thr Lys Gly Ala Gly Lys
 265     270     275
Lys Lys
 280     285     290

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<210> 62

<211> 552

<212> PRT

<213> Oryza sativa

<220>

<221> PEPTIDE

<222> (0)...(0)

<223> line 1C-064-20 polypeptide sequence

<400> 62

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Met Ala Ser Ala Pro Gly Asp Gly Lys Gln Gly Gly Gly Gly Gly
 1      5      10      15
Pro Ala Val Gly Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Ala Val
 20      25      30
Trp Arg His Asp Arg Gly Glu Val Ile Ala Asn Asp Gln Arg Asn Arg
 35      40      45
Leu Thr Pro Ser Cys Val Ala Phe Thr Ala Asp Asp Asp Ser Phe
 50      55      60

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Val 65	Gly	Asp	Ala	Ala	Phe 70	Asn	Gln	Ser	Ala	Leu 75	Asn	Pro	Thr	Asn	Thr 80
Ile	Phe	Glu	Val	Lys 85	Arg	Leu	Ile	Gly	Arg 90	Arg	Phe	Ser	Asp	Asp 95	Ser
Val	Gln	Lys	Asp 100	Ile	Lys	Leu	Trp	Pro 105	Phe	Lys	Val	Val	Ala 110	Gly	Gln
Glu	Asp	Arg	Pro	Met	Ile	Val	Val	Arg	His	Glu	Gly	Glu	Glu	Arg	Gln
Phe	Met 115	Pro	Glu	Glu	Ile	Ser	Ser	Met	Val	Leu	Ala 125	Lys	Met	Arg	Glu
Thr 130	Ala	Glu	Val	Tyr	Leu 135	Gly	Lys	Thr	Val	Thr	Lys	Ala	Val	Ile	Thr
145	Pro	Val	Tyr	Phe 150	Asn	Asn	Ala	Gln	Arg	Gln	Ala	Thr	Met	Asp	Ala
Val	Pro	Val	Tyr	Phe 165	Asn	Asn	Ala	Gln	Arg	Gln	Ala	Thr	Met	Asp	Ala
Gly	Ala	Ile	Ala	Gly 180	Leu	Asn	Val	Met	Arg	Ile	Ile	Asn	Glu	Pro	Thr
Ala	Ala	Ala	Leu	Ala	Tyr	Cys	Leu 185	Glu	Lys	Met	Pro	Val	Ser	Asn	Lys
195	Arg	Met	Val	Leu	Val	Phe	Asp 200	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Ile
Gly 210	Arg	Met	Val	Leu	Val	Phe	Asp 215	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Ile
Ser 225	Leu	Leu	Asn	Ile	Asp 230	Pro	Gly	Glu	Gly	Thr	Ala	Gly	Asp	Thr	His
225	Leu	Leu	Asn	Ile	Asp 230	Pro	Gly	Glu	Gly	Thr	Ala	Gly	Asp	Thr	His
Leu	Gly	Gly	Ala	Asp 245	Phe	Asp	Asn	Glu	Leu	Val	Lys	His	Ser	Leu	Arg
245	Glu	Phe	Asn	Arg 260	Lys	His	Gly	Ser	Met	Asp	Ile	Glu	Ser	Asn	Gln
Glu	Phe	Asn	Arg 260	Lys	His	Gly	Ser	Met	Asp	Ile	Glu	Ser	Asn	Gln	Lys
Ala	Leu	Arg	Arg 275	Leu	Arg	Thr	Ala 280	Cys	Glu	Arg	Ala	Lys	Arg	Met	Leu
275	Ser	Ser	Thr	Met	Gln	Thr	Thr 295	Ile	Glu	Val	Asp	Ser	Leu	His	Gln
Ser 290	Ser	Thr	Met	Gln	Thr	Thr 295	Ile	Glu	Val	Asp	Ser	Leu	His	Gln	Gly
Ile 305	Asp	Phe	Arg	Val	Thr 310	Leu	Thr	Arg	Ser	Arg 315	Phe	Glu	Glu	Leu	Asn
305	Asp	Phe	Arg	Val	Thr 310	Leu	Thr	Arg	Ser	Arg 315	Phe	Glu	Glu	Leu	Asn
Lys	Asp	Leu	Phe	Ser 325	Lys	Cys	Met	Glu	Ala 330	Met	Glu	Asn	Cys	Leu	Arg
Lys	Asp	Leu	Phe	Ser 325	Lys	Cys	Met	Glu	Ala 330	Met	Glu	Asn	Cys	Leu	Arg
Asp	Ala	Lys	Val	Asp 340	Lys	Trp	Ser	Val	Asp 345	Asp	Val	Val	Leu	Val	Gly
340	Gly	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln 360	Lys	Met	Leu	Ser	Glu	Phe
Gly 355	Ser	Thr	Arg	Ile	Pro	Lys	Val	Gln 360	Lys	Met	Leu	Ser	Glu	Phe	Phe
355	Asp	Gly	Lys	Glu	Leu	Cys	Arg 375	Ser	Ile	Asn	Pro	Asp 380	Glu	Ala	Val
Asp 370	Gly	Lys	Glu	Leu	Cys	Arg 375	Ser	Ile	Asn	Pro	Asp 380	Glu	Ala	Val	Ala
Tyr 385	Gly	Ala	Ala	Ile	Gln 390	Ala	Ser	Ile	Leu	Cys 395	Gly	Gly	Thr	Asp	Asp
385	Gly	Ala	Ala	Ile	Gln 390	Ala	Ser	Ile	Leu	Cys 395	Gly	Gly	Thr	Asp	Asp
Lys	Arg	Leu	Val	Asp 405	Met	Leu	Leu	Arg	Glu	Val	Thr	Pro	Leu	Ser	Leu
Lys	Arg	Leu	Val	Asp 405	Met	Leu	Leu	Arg	Glu	Val	Thr	Pro	Leu	Ser	Leu
Gly	Val	Glu	Thr 420	Glu	Asp	Asn	Cys	Thr 425	Met	Ser	Val	Val	Ile	Pro	Arg
420	Gly	Val	Glu	Thr 420	Glu	Asp	Asn	Cys	Thr 425	Met	Ser	Val	Val	Ile	Pro
Asn	Thr	Ala	Ile	Pro	Thr	Lys	Lys 440	Val	Lys	Asn	Phe	Thr	Thr	Leu	Tyr
435	Asn	Thr	Ala	Ile	Pro	Thr	Lys 440	Val	Lys	Asn	Phe	Thr	Thr	Leu	Tyr
Asp 450	Asn	Gln	Ile	Asn	Val	Ser 455	Phe	Pro	Val	Tyr	Glu	Gly	Glu	Ser	Ala
450	Asn	Gln	Ile	Asn	Val	Ser 455	Phe	Pro	Val	Tyr	Glu	Gly	Glu	Ser	Ala
Asn 465	Thr	Lys	Asp	Asn	Asn 470	Leu	Leu	Gly	Glu	Phe	Thr	Leu	Tyr	Gly	Ile
465	Thr	Lys	Asp	Asn	Asn 470	Leu	Leu	Gly	Glu	Phe	Thr	Leu	Tyr	Gly	Ile
Pro	Pro	Ala	Pro	Lys 485	Arg	Val	Pro	Ser	Ile	Asp	Val	Thr	Phe	Asp	Ile
Pro	Pro	Ala	Pro	Lys 485	Arg	Val	Pro	Ser	Ile	Asp	Val	Thr	Phe	Asp	Ile
Asp	Ala	Asn	Gly 500	Val	Leu	Asn	Val	Ser 505	Ala	Glu	His	Lys	Val	Thr	Gly
Asp	Ala	Asn	Gly 500	Val	Leu	Asn	Val	Ser 505	Ala	Glu	His	Lys	Val	Thr	Gly
Gln	Lys	Asn 515	Ser	Ile	Thr	Ile	Thr 520	Asn	Arg	Ser	Gly	Arg 525	Leu	Asn	Gln
515	Gln	Lys	Asn 515	Ser	Ile	Thr	Ile 520	Asn	Arg	Ser	Gly	Arg 525	Leu	Asn	Gln
Glu	Glu	Ile	Asp	Arg	Met	Ala 535	Leu	Glu	Pro	Glu	Arg	His	Lys	Met	Lys
530	Glu	Glu	Ile	Asp	Arg	Met 535	Leu	Glu	Pro	Glu	Arg	His	Lys	Met	Lys
Arg 545	Ile	Lys	Leu	His	Glu 550	Val	Val								
545	Ile	Lys	Leu	His	Glu 550	Val	Val								

<210> 63
 <211> 479
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-109-35 polypeptide sequence

<400> 63
 Met Ser Ser Ser Ala Thr Val Val Pro Leu Ala Tyr Gln Gly Asn Thr
 1 5 10 15
 Ser Ala Ser Val Ala Asp Trp Leu Asn Lys Gly Asp Asn Ala Trp Gln
 20 25 30
 Leu Val Ala Ala Thr Leu Val Gly Leu Gln Ser Val Pro Gly Leu Val
 35 40 45
 Val Leu Tyr Gly Gly Val Val Lys Lys Lys Trp Ala Val Asn Ser Ala
 50 55 60
 Phe Met Ala Leu Tyr Ala Phe Ala Ala Val Trp Ile Cys Trp Val Thr
 65 70 75 80
 Trp Ala Tyr Asn Met Ser Phe Gly Glu Lys Leu Leu Pro Ile Trp Gly
 85 90 95
 Lys Ala Arg Pro Ala Leu Asp Gln Gly Leu Leu Val Gly Arg Ala Ala
 100 105 110
 Leu Pro Ala Thr Val His Tyr Arg Ala Asp Gly Ser Val Glu Thr Ala
 115 120 125
 Ala Val Glu Pro Leu Tyr Pro Met Ala Thr Val Val Tyr Phe Gln Cys
 130 135 140
 Val Phe Ala Ala Ile Thr Leu Ile Leu Val Ala Gly Ser Leu Leu Gly
 145 150 155 160
 Arg Met Ser Phe Leu Ala Trp Met Ile Phe Val Pro Leu Trp Leu Thr
 165 170 175
 Phe Ser Tyr Thr Val Gly Ala Phe Ser Leu Trp Gly Gly Gly Phe Leu
 180 185 190
 Phe His Trp Gly Val Ile Asp Tyr Cys Gly Gly Tyr Val Ile His Val
 195 200 205
 Ser Ala Gly Ile Ala Gly Phe Thr Ala Ala Tyr Trp Val Gly Pro Arg
 210 215 220
 Ala Gln Lys Asp Arg Glu Arg Phe Pro Pro Asn Asn Ile Leu Phe Thr
 225 230 235 240
 Leu Thr Gly Ala Gly Leu Leu Trp Met Gly Trp Ala Gly Phe Asn Gly
 245 250 255
 Gly Gly Pro Tyr Ala Ala Asn Ser Val Ala Ser Met Ala Val Leu Asn
 260 265 270
 Thr Asn Ile Cys Thr Ala Met Ser Leu Ile Val Trp Thr Cys Leu Asp
 275 280 285
 Val Ile Phe Phe Lys Lys Pro Ser Val Val Gly Ala Val Gln Gly Met
 290 295 300
 Ile Thr Gly Leu Val Cys Ile Thr Pro Ala Ala Gly Val Val Gln Gly
 305 310 315 320
 Trp Ala Ala Leu Val Met Gly Val Leu Ala Gly Ser Ile Pro Trp Tyr
 325 330 335
 Thr Met Met Ile Leu His Lys Arg Ser Lys Ile Leu Gln Arg Val Asp
 340 345 350
 Asp Thr Leu Gly Val Phe His Thr His Gly Val Ala Gly Leu Leu Gly
 355 360 365
 Gly Leu Leu Thr Gly Leu Phe Ala Glu Pro Thr Leu Cys Asn Leu Phe
 370 375 380
 Leu Pro Val Ala Asp Ser Arg Gly Ala Phe Tyr Gly Gly Ala Gly Gly
 385 390 395 400
 Ala Gln Phe Gly Lys Gln Ile Ala Gly Gly Leu Phe Val Val Ala Trp

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405
 Asn Val Val Val Thr Ser Leu Ile Cys Leu Ala Ile Asn Leu Leu Val
 420
 Pro Leu Arg Met Pro Asp Asp Lys Leu Glu Val Gly Asp Asp Ala Val
 435
 His Gly Glu Glu Ala Tyr Ala Leu Trp Gly Asp Gly Glu Met Tyr Asp
 450
 Val Thr Lys His Gly Ser Asp Ala Ala Val Ala Pro Val Val Val
 465 470 475

<210> 64
 <211> 2177
 <212> PRT
 <213> Oryza sativa

<220>
 <221> PEPTIDE
 <222> (0)...(0)
 <223> line 1C-109-51 polypeptide sequence

<400> 64
 Met Ala Asn Leu Gly Gly Gly Ala Glu Ala His Ala Arg Phe Lys Gln
 1 5 10 15
 Tyr Glu Tyr Arg Ala Asn Ser Ser Leu Val Leu Thr Thr Asp Ser Arg
 20 25 30
 Pro Arg Asp Thr His Glu Pro Thr Gly Glu Pro Glu Thr Leu Trp Gly
 35 40 45
 Arg Ile Asp Pro Arg Ser Phe Gly Asp Arg Ala Val Gln Ala Lys Pro
 50 55 60
 Pro Glu Leu Glu Glu Lys Leu Thr Lys Ser Arg Lys Lys Lys Ala Ala
 65 70 75 80
 Ala Ser Asp Pro Asp Leu His Arg Arg Asp Ala Lys Arg Arg Arg
 85 90 95
 Arg Ala Ala Ala Ala Gln Ser Glu Val Ser Val Leu Ser Leu Thr Asp
 100 105 110
 Asp Val Val Tyr Lys Pro Gln Thr Lys Glu Thr Arg Ala Ala Tyr Glu
 115 120 125
 Ala Leu Leu Ser Val Ile Gln Gln Phe Gly Gly Gln Pro Leu Asp
 130 135 140
 Val Leu Gly Gly Ala Ala Asp Glu Val Leu Ala Val Leu Lys Asn Asp
 145 150 155 160
 Lys Ile Lys Ser Pro Asp Lys Lys Lys Glu Ile Glu Lys Leu Leu Asn
 165 170 175
 Pro Ile Ser Asn Gln Met Phe Asp Gln Ile Val Ser Ile Gly Lys Leu
 180 185 190
 Ile Thr Asp Phe His Asp Ala Ser Ala Gly Asp Ser Ala Ala Ala Pro
 195 200 205
 Ser Gly Asp Gly Met Asp Thr Ala Leu Asp Asp Asp Ile Gly Val Ala
 210 215 220
 Val Glu Phe Glu Glu Asn Glu Asp Asp Glu Glu Ser Asp Phe Asp Gln
 225 230 235 240
 Val Gln Asp Asp Leu Asp Glu Asp Glu Asp Asp Asp Leu Pro Glu Ser
 245 250 255
 Asn Ala Pro Gly Ala Met Gln Met Gly Gly Glu Leu Asp Asp Asp Asp
 260 265 270
 Met Gln Asn Ser Asn Glu Gly Leu Thr Ile Asn Val Gln Asp Ile Asp
 275 280 285
 Ala Tyr Trp Leu Gln Arg Lys Val Ser Gln Ala Tyr Glu Asp Ile Asp
 290 295 300
 Pro Gln His Ser Gln Lys Leu Ala Glu Glu Ile Leu Lys Ile Ile Ala
 305 310 315 320
 Glu Gly Asp Asp Arg Asp Val Glu Asn Arg Leu Val Met Leu Leu Asp

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Glu Glu Leu Phe Ala Asp Lys His Ile Gln Val Leu Val Ser Thr Ala
 835 840 845
 Thr Leu Ala Trp Gly Val Asn Leu Pro Ala His Thr Val Ile Ile Lys
 850 855 860
 Gly Thr Gln Ile Tyr Asn Pro Glu Lys Gly Ala Trp Thr Glu Leu Ser
 865 870 875 880
 Pro Leu Asp Val Met Gln Met Leu Gly Arg Ala Gly Arg Pro Gln Tyr
 885 890 895
 Asp Thr His Gly Glu Gly Ile Ile Leu Thr Gly His Ser Glu Leu Gln
 900 905 910
 Tyr Tyr Leu Ser Leu Met Asn Gln Gln Leu Pro Ile Glu Ser Gln Phe
 915 920 925
 Ile Ser Arg Leu Ala Asp Gln Leu Asn Ala Glu Ile Val Leu Gly Thr
 930 935 940
 Ile Gln Asn Ala Arg Glu Ala Cys Ser Trp Leu Gly Tyr Thr Tyr Leu
 945 950 955 960
 Tyr Ile Arg Met Leu Arg Asn Pro Thr Leu Tyr Gly Leu Pro Ala Asp
 965 970 975
 Ile Met Glu Thr Asp Lys Thr Leu Asp Glu Arg Arg Ala Asp Leu Val
 980 985 990
 His Ser Ala Asn Leu Leu Asp Arg Asn Asn Leu Ile Lys Tyr Asp
 995 1000 1005
 Arg Lys Thr Gly Tyr Phe Gln Val Thr Asp Leu Gly Arg Ile Ala Ser
 1010 1015 1020
 Tyr Tyr Tyr Ile Ser His Gly Thr Ile Ser Thr Tyr Asn Glu Tyr Leu
 1025 1030 1035 1040
 Lys Pro Thr Met Gly Asp Ile Glu Leu Cys Arg Leu Phe Ser Leu Ser
 1045 1050 1055
 Glu Glu Phe Lys Tyr Val Ser Val Arg Gln Asp Glu Lys Met Glu Leu
 1060 1065 1070
 Ala Lys Leu Leu Asp Arg Val Pro Ile Pro Val Lys Glu Ser Leu Glu
 1075 1080 1085
 Glu Pro Ser Ala Lys Ile Asn Val Leu Leu Gln Ala Tyr Ile Ser Arg
 1090 1095 1100
 Leu Lys Leu Glu Gly Leu Ser Leu Ser Ser Asp Met Val Tyr Ile Arg
 1105 1110 1115 1120
 Gln Ser Ala Gly Arg Leu Leu Arg Ala Leu Phe Glu Ile Val Leu Lys
 1125 1130 1135
 Arg Gly Trp Ala Gln Leu Ala Glu Lys Ala Leu Asn Leu Cys Lys Met
 1140 1145 1150
 Ile Asp Lys Gln Met Trp Asn Val Gln Thr Pro Leu Arg Gln Phe Pro
 1155 1160 1165
 Gly Ile Pro Lys Glu Ile Leu Met Lys Leu Glu Lys Lys Glu Leu Ala
 1170 1175 1180
 Trp Glu Arg Tyr Tyr Asp Leu Ser Ser Gln Glu Ile Gly Glu Leu Ile
 1185 1190 1195 1200
 Arg Phe Pro Lys Met Gly Arg Gln Leu His Lys Cys Ile His Gln Leu
 1205 1210 1215
 Pro Lys Leu Asn Leu Ser Ala His Val Gln Pro Ile Thr Arg Thr Val
 1220 1225 1230
 Leu Gly Phe Glu Leu Thr Ile Thr Pro Asp Phe Gln Trp Asp Asp Lys
 1235 1240 1245
 Val His Gly Tyr Val Glu Pro Phe Trp Val Ile Val Glu Asp Asn Asp
 1250 1255 1260
 Gly Glu Asn Ile Leu His Glu Tyr Phe Met Val Lys Lys Gln Tyr
 1265 1270 1275 1280
 Val Asp Glu Asp His Thr Leu Asn Phe Thr Val Pro Ile Tyr Glu Pro
 1285 1290 1295
 Leu Pro Pro Gln Tyr Phe Ile Arg Val Val Ser Asp Lys Trp Leu Gly
 1300 1305 1310
 Ser Gln Thr Ile Leu Pro Val Cys Phe Arg His Leu Ile Leu Pro Glu
 1315 1320 1325
 Lys Tyr Ala Pro Pro Thr Glu Leu Leu Asp Leu Gln Pro Leu Pro Val

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1330	1335	1340
Thr Ala Leu Arg Asn	Ala Arg Tyr Glu Gly	Leu Tyr Ser Ala Phe Lys
1345	1350	1355
His Phe Asn Pro Ile	Gln Thr Gln Val Phe Thr Val	Leu Tyr Asn Thr
1365	1370	1375
Asp Asp Ser Val Leu Val	Ala Ala Pro Thr Gly Ser Gly	Lys Thr Ile
1380	1385	1390
Cys Ala Glu Phe Ala Ile	Leu Arg Asn His Gln Lys	Ala Val Ser Gly
1395	1400	1405
Glu Ser Asn Met Arg Val	Val Tyr Ile Ala Pro Ile	Glu Ala Leu Ala
1410	1415	1420
Lys Glu Arg Tyr Arg Asp	Trp Glu Gln Lys Phe Gly	Glu Phe Ala Arg
1425	1430	1435
Val Val Glu Leu Thr Gly	Glu Thr Ala Ala Asp	Leu Lys Leu Asp
1445	1450	1455
Lys Gly Glu Ile Ile Ile	Ser Thr Pro Glu Lys Trp Asp	Ala Leu Ser
1460	1465	1470
Arg Arg Trp Lys Gln Arg	Lys Gln Val Gln Gln Val	Ser Leu Phe Ile
1475	1480	1485
Val Asp Glu Leu His Leu	Ile Gly Ser Glu Lys Gly	His Val Leu Glu
1490	1495	1500
Val Ile Val Ser Arg Met	Arg Arg Ile Ala Ser His	Ile Gly Ser Asn
1505	1510	1515
Ile Arg Ile Val Ala Leu	Ser Ala Ser Leu Ala Asn	Ala Lys Asp Leu
1525	1530	1535
Gly Glu Trp Ile Gly Ala	Thr Ser His Gly Leu Phe	Asn Phe Pro Pro
1540	1545	1550
Ala Val Arg Pro Val Pro	Leu Glu Ile His Ile Gln	Gly Val Asp Ile
1555	1560	1565
Ala Asn Phe Glu Ala Arg	Met Gln Ala Met Thr Lys	Pro Thr Tyr Thr
1570	1575	1580
Ala Ile Thr Gln His Ala	Lys Asn Gly Lys Pro Ala	Leu Val Phe Val
1585	1590	1595
Pro Thr Arg Lys His Ala	Arg Leu Thr Ala Leu Asp	Leu Cys Ala Tyr
1605	1610	1615
Ser Ser Ala Glu Gly Gly	Gly Thr Pro Phe Leu Leu	Gly Ser Glu Asp
1620	1625	1630
Glu Met Asp Ala Phe Thr	Gly Gly Ile Ser Asp Glu	Thr Leu Lys Tyr
1635	1640	1645
Thr Leu Lys Cys Gly Val	Gly Tyr Leu His Glu Gly	Leu Ser Asp Leu
1650	1655	1660
Glu Gln Glu Val Val Thr	Gln Leu Phe Leu Ser Gly	Arg Ile Gln Val
1665	1670	1675
Cys Val Ala Ser Ser Thr	Val Cys Trp Gly Arg Ser	Leu Pro Ala His
1685	1690	1695
Leu Val Val Val Met Gly	Thr Gln Tyr Tyr Asp Gly	Arg Glu Asn Ala
1700	1705	1710
His Thr Asp Tyr Pro Ile	Thr Asp Leu Leu Gln Met	Met Gly His Ala
1715	1720	1725
Ser Arg Pro Leu Gln Asp	Asn Ser Gly Lys Cys Val	Ile Leu Cys His
1730	1735	1740
Ala Pro Arg Lys Glu Tyr	Tyr Lys Lys Phe Leu Phe	Glu Ala Phe Pro
1745	1750	1755
Val Glu Ser His Leu His	His Phe Leu His Asp	His Met Asn Ala Glu
1765	1770	1775
Val Val Val Gly Val Ile	Glu Asn Lys Gln Asp	Ala Val Asp Tyr Leu
1780	1785	1790
Thr Trp Thr Phe Met Tyr	Arg Arg Leu Thr Lys Asn	Pro Asn Tyr Tyr
1795	1800	1805
Asn Leu Gln Gly Val Ser	His Arg His Leu Ser Asp	His Leu Ser Glu
1810	1815	1820
Leu Val Glu Thr Val Leu	Asn Asp Leu Glu Ser Ser	Lys Cys Val Ala
1825	1830	1835
		1840

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Ile Glu Glu Asp Met Tyr Leu Lys Pro Leu Asn Leu Gly Leu Ile Ala
 1845 1850 1855
 Ser Tyr Tyr Tyr Ile Ser Tyr Thr Thr Ile Glu Arg Phe Ser Ser Met
 1860 1865 1870
 Leu Thr Gln Lys Thr Lys Met Lys Gly Leu Leu Glu Ile Leu Ala Ser
 1875 1880 1885
 Ala Ser Glu Tyr Ala Glu Leu Pro Ser Arg Pro Gly Glu Glu Asp Phe
 1890 1895 1900
 Ile Glu Lys Leu Val Arg His Gln Arg Phe Ser Ile Glu Lys Pro Arg
 1905 1910 1915 1920
 Tyr Gly Asp Pro His Val Lys Ala Asn Ala Leu Leu Gln Ala His Phe
 1925 1930 1935
 Ser Arg His Thr Ile Leu Gly Asn Leu Ala Ala Asp Gln Arg Glu Ile
 1940 1945 1950
 Leu Leu Ser Ala His Arg Leu Leu Gln Ala Met Val Asp Val Ile Ser
 1955 1960 1965
 Ser Asn Gly Trp Leu Thr Leu Ala Leu Asn Ala Met Glu Leu Ser Gln
 1970 1975 1980
 Met Val Thr Gln Gly Met Trp Asp Arg Asp Ser Val Leu Leu Gln Leu
 1985 1990 1995 2000
 Pro His Phe Thr Lys Glu Leu Ala Arg Arg Cys Gln Glu Asn Glu Gly
 2005 2010 2015
 Arg Pro Ile Glu Ser Ile Phe Asp Leu Ala Glu Met Ser Ile Asp Glu
 2020 2025 2030
 Met Arg Asp Leu Leu Gln Gln Ser Asn Pro Gln Leu Gln Asp Ile Ile
 2035 2040 2045
 Glu Phe Phe Lys Arg Phe Pro Asn Val Asp Met Ala Tyr Glu Val Arg
 2050 2055 2060
 Glu Gly Asp Asp Ile Arg Ala Gly Asp Asn Val Thr Val Gln Val Thr
 2065 2070 2075 2080
 Leu Glu Arg Asp Met Thr Asn Leu Pro Ser Glu Val Gly Pro Val His
 2085 2090 2095
 Ala Pro Arg Tyr Pro Lys Pro Lys Glu Gly Trp Trp Leu Val Ile
 2100 2105 2110
 Gly Asp Ser Ser Thr Asn Gln Leu Leu Ala Ile Lys Arg Val Ala Leu
 2115 2120 2125
 Gln Lys Arg Ala Arg Val Lys Leu Glu Phe Thr Ala Ala Ser Glu Ala
 2130 2135 2140
 Gly Arg Lys Glu Tyr Met Ile Tyr Leu Met Ser Asp Ser Tyr Leu Gly
 2145 2150 2155 2160
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 2165 2170 2175
 Asp

<210> 65
 <211> 181
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (0)...(0)
 <223> line 1C-056-07 polypeptide sequence

<400> 65
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 Leu Leu His Gly Tyr Lys Phe Asp Ser Ile Asn Thr Val Tyr Tyr Met
 20 25 30
 Ala Pro Phe Ala Thr Met Ile Leu Ala Leu Pro Ala Val Leu Leu Glu
 35 40 45

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Gly Gly Gly Val Val Thr Trp Phe Tyr Thr His Asp Ser Ile Ala Ser
 50 55 60
 Ala Leu Val Ile Ile Ile Gly Ser Gly Val Leu Ala Phe Cys Leu Asn
 65 70 75 80
 Phe Ser Ile Phe Tyr Val Ile His Ser Thr Thr Ala Val Thr Phe Asn
 85 90 95
 Val Ala Gly Asn Leu Lys Val Ala Val Ala Val Leu Val Ser Trp Leu
 100 105 110
 Ile Phe Arg Asn Pro Ile Ser Pro Met Asn Ala Ile Gly Cys Ala Ile
 115 120 125
 Thr Leu Val Gly Cys Thr Phe Tyr Gly Tyr Val Arg His Leu Ile Ser
 130 135 140
 Gln Gln Gln Ala Val Ala Pro Gly Thr Gly Ser Pro Thr Thr Ser Gln
 145 150 155 160
 Thr Asn Ser Pro Arg Ser Arg Met Glu Met Leu Pro Leu Val Gly Asp
 165 170 175
 Lys Gln Glu Lys Val
 180

<210> 66
 <211> 793
 <212> PRT
 <213> Oryza sativa

<220>
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 Met Glu Ser Asp Val Ala Glu Glu Lys Arg Lys Arg Glu Asp Asp Ala
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 Ser Ser Ser Ala Val Leu Ala Ala Ala Asn Asn Thr Gly Gly Ala Gln
 35 40 45
 His Pro Met Trp Lys Thr Ser Leu Cys Ser Phe Phe Arg Arg Arg Ala
 50 55 60
 Ala Ser Ser Ala Asp Gly Cys Ser His Gly Asp Ser Cys Arg Tyr Ala
 65 70 75 80
 His Ser Glu Glu Glu Leu Arg Pro Arg Pro Asp Gly Thr Trp Asp Pro
 85 90 95
 Thr Ser Asp Arg Ala Lys Lys Leu Arg Lys Val Ala Ala Asp Glu Val
 100 105 110
 Glu Glu Glu Val Val Thr Ile Asp Asp Lys Ala Leu Asp Lys Cys Leu
 115 120 125
 Val Gly Leu Pro Arg Gly Trp Ala Asn Asp Arg Leu Lys Thr Phe Leu
 130 135 140
 Gln Asp Lys Ala Arg Thr Asn Tyr Ser Ser Ile Leu Pro Pro Ala Leu
 145 150 155 160
 Leu Leu Gly Ile Ser Tyr Ala Thr Ala Lys Lys Lys Lys Gly Met Thr
 165 170 175
 Val Gly Phe Val Thr Phe Glu Asn Ile Glu Gln Leu Lys Asn Ala Ile
 180 185 190
 Glu Val Leu Thr Glu Asn Gln Ser Gly Gly Lys Glu Ile Lys Ile Ala
 195 200 205
 Asp Ala Asn Arg Arg Ser His Gln Lys Leu His Thr Glu Lys Pro Val
 210 215 220
 Ser Asp Asn Gly Val Thr Thr Glu Asn Gly Thr Ser Val Asp Val Pro
 225 230 235 240
 Pro Gly Glu Thr Ser Ala Pro Glu Ala Ala Ile Ser Asn Lys Lys Ser
 245 250 255

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Val	Arg	Asp	Ala	Val	Thr	Pro	Leu	Ala	His	Met	Ser	Tyr	Asn	Asp	Gln
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Leu	Glu	His	Lys	Asn	Asn	Ser	Val	Ala	Gln	Ile	Leu	Lys	Arg	Leu	Thr
		275					280					285			
Arg	Asn	Ala	Arg	Lys	Ala	Cys	Pro	Thr	Gly	Ile	Pro	Leu	Pro	Asp	Trp
	290					295					300				
Val	Phe	Lys	Ser	Lys	Glu	Ile	Gly	Gly	Leu	Pro	Cys	Lys	Leu	Glu	Gly
305					310					315				320	
Ile	Leu	Glu	Ser	Pro	Val	Ile	Asn	Gly	Tyr	Arg	Asn	Lys	Cys	Glu	Phe
				325					330					335	
Ser	Val	Gly	Phe	Ser	Leu	Glu	Gly	Lys	Lys	Thr	Val	Gly	Phe	Met	Leu
			340					345					350		
Gly	Asn	Phe	Ser	Thr	Asp	Met	Ile	Asp	Lys	Thr	Lys	Ser	Arg	Glu	Gly
		355					360					365			
Val	Thr	Ala	Val	Glu	Glu	Pro	Val	Asp	Cys	Pro	Asn	Val	Ser	Glu	Ile
						375					380				
Ser	Cys	Lys	Tyr	Ala	Leu	Met	Phe	Gln	Asp	Phe	Leu	Gln	Ser	Ser	Ser
385					390					395					400
Leu	Pro	Val	Trp	Asn	Arg	Val	Asn	Asn	Cys	Gly	Phe	Trp	Arg	Gln	Phe
				405					410					415	
Thr	Val	Arg	Glu	Gly	Arg	Cys	Arg	Ala	Gln	Ala	Val	Ala	Gln	Asn	Ala
			420					425					430		
Glu	Thr	Gln	Ile	Ser	Glu	Val	Met	Leu	Ile	Val	Gln	Val	Cys	Ser	Thr
			435				440					445			
Gly	Val	Asp	Asp	Ala	Val	Met	Lys	Asp	Glu	Phe	Asp	Lys	Leu	Thr	Val
	450					455					460				
Ala	Leu	Gln	Gln	Gly	Ala	Ala	Thr	Cys	Ser	Pro	Pro	Leu	Pro	Leu	Thr
465					470					475					480
Thr	Ile	Val	Val	Gln	Asp	His	Lys	Gly	Ile	Ser	Asn	Ala	Ala	Pro	Ala
				485					490					495	
Asp	Cys	Pro	Leu	Ile	Pro	Leu	Leu	Val	Pro	Lys	Val	Asp	Gln	Ser	Glu
			500					505					510		
Gly	Thr	Val	Asp	Lys	Thr	Arg	Ile	His	Asp	His	Ile	Gly	Asn	Leu	Trp
		515					520					525			
Phe	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Phe	Gln	Val	Asn	Thr	Leu	Ala	Ala
	530					535					540				
Glu	Arg	Leu	Tyr	Thr	Leu	Ala	Gly	Asp	Trp	Ala	Asn	Leu	Asn	Ser	Gly
545					550					555					560
Thr	Leu	Leu	Phe	Asp	Val	Cys	Cys	Gly	Thr	Gly	Thr	Ile	Gly	Leu	Thr
				565					570					575	
Leu	Ala	His	Arg	Val	Gly	Met	Val	Val	Gly	Ile	Glu	Met	Asn	Glu	Ser
			580					585					590		
Ala	Val	Ser	Asp	Ala	Glu	Arg	Asn	Ala	Leu	Ile	Asn	Gly	Val	Ser	Asn
		595					600					605			
Cys	Arg	Phe	Val	Cys	Gly	Lys	Ala	Glu	Asp	Val	Met	Gly	Ser	Leu	Leu
	610					615					620				
Thr	Glu	Tyr	Leu	Gly	Ser	Pro	Gln	Gln	Asp	Ile	Pro	Val	Ser	Glu	Gly
625					630					635					640
Ala	Val	Ser	Gly	Thr	Val	Lys	Asp	Glu	Glu	Val	Ile	Asp	Ser	Ser	Lys
				645					650					655	
Asn	Ser	Gly	Glu	Asn	Leu	Asp	Ser	Ser	Met	Gln	Lys	Asn	Asp	Asn	Gly
			660					665					670		
Lys	Ser	Gln	Gln	Leu	Gly	Asp	Ala	Pro	Ala	Asp	Ser	Ser	Ser	Ser	Ala
		675					680					685			
Ile	Asp	Glu	Ile	Lys	Gly	Asn	Ser	Asn	Asp	Arg	Val	Gly	Asn	Gly	Leu
	690					695					700				
Glu	Gly	Ser	His	Asp	Glu	Tyr	Asn	Glu	Val	Ala	Gly	Glu	Asp	Ile	His
705					710					715					720
Gly	Glu	Ala	Ser	Leu	Ile	Asn	Glu	Ser	Val	Asp	Leu	Lys	Val	Ser	Asp
				725					730					735	
Cys	Leu	Glu	Asp	Arg	Lys	Thr	Ser	Asp	Gly	Ser	Ser	Ile	Ser	Ser	Asn
			740					745				750			
Asn	Asp	Val	Thr	Ala	Ala	Thr	Ala	Cys	Gln	Phe	Glu	Asp	Ile	Val	Ala

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Ile Val Asp Pro Pro Arg Val Gly Leu His Pro Thr Val Asn Pro Lys
 755 760 765
 770 775 780
 Arg Gly Gln Gly Val Pro Val Phe Ile
 785 790

<210> 67
 <211> 143
 <212> PRT
 <213> Oryza sativa

<220>
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 <223> line 1C-142-27 polypeptide sequence

<400> 67
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 20 25 30
 Phe Val Val Tyr Lys Ile Asp Glu Arg Ser Arg Ala Val Leu Val Asp
 35 40 45
 Lys Val Gly Gly Pro Gly Glu Gly Tyr Glu Glu Leu Val Ala Ala Leu
 50 55 60
 Pro Thr Asp Asp Cys Arg Tyr Ala Val Phe Asp Phe Asp Phe Val Thr
 65 70 75 80
 Val Asp Asn Cys Gln Lys Ser Lys Ile Phe Phe Ile Ala Trp Ser Pro
 85 90 95
 Thr Ala Ser Arg Ile Arg Ala Lys Ile Leu Tyr Ala Thr Ser Lys Gln
 100 105 110
 Gly Leu Arg Arg Val Leu Asp Gly Val His Tyr Glu Val Gln Ala Thr
 115 120 125
 Asp Ser Ser Glu Met Gly Tyr Asp Val Ile Arg Gly Arg Ala Gln
 130 135 140

<210> 68
 <211> 452
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (0)...(0)
 <223> line 1C-140-04 polypeptide sequence

<400> 68
 Met Ala Thr Gly Glu Leu Ala Leu Val Ser Ser Leu Phe Ile Val Val
 1 5 10
 Val Phe Leu Leu Leu Gly Ala Val Ala Arg Glu Ala Ser Ala Leu Thr
 20 25 30
 Arg His Asp Phe Pro Glu Gly Phe Val Phe Gly Ala Gly Ser Ser Ala
 35 40 45
 Phe Gln Val Glu Gly Ala Ala Glu Asp Gly Arg Lys Pro Ser Ile
 50 55 60
 Trp Asp Thr Phe Ile His Gln Gly Tyr Met Pro Asp Gly Ser Asn Ala
 65 70 75 80
 Asp Val Ser Ala Asp Gln Tyr His His Tyr Lys Glu Asp Val Lys Leu
 85 90 95
 Met Tyr Asp Met Gly Leu Asp Ala Tyr Arg Phe Ser Ile Ala Trp Pro
 100 105 110

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Arg Leu Ile Pro Asp Gly Arg Gly Glu Ile Asn Pro Lys Gly Leu Glu
 115 120 125
 Tyr Tyr Asn Asn Leu Ile Asp Glu Leu Ile Met His Gly Ile Gln Pro
 130 135 140
 His Val Thr Ile Tyr His Phe Asp Leu Pro Gln Ala Leu Gln Asp Glu
 145 150 155 160
 Tyr Gly Gly Ile Leu Ser Pro Arg Phe Ile Glu Asp Tyr Ser Ala Tyr
 165 170 175
 Ala Glu Val Cys Phe Lys Asn Phe Gly Asp Arg Val Lys His Trp Ala
 180 185 190
 Thr Phe Asn Gln Pro Asn Ile Glu Pro Ile Gly Gly Phe Asp Ala Gly
 195 200 205
 Asp Arg Pro Pro Arg Arg Cys Ser Tyr Pro Phe Gly Thr Asn Cys Thr
 210 215 220
 Gly Gly Asp Ser Ser Thr Glu Pro Tyr Ile Val Ala His His Leu Leu
 225 230 235 240
 Leu Ala His Ala Ser Ala Val Ser Ile Tyr Arg Gln Lys Tyr Gln Gln
 245 250 255
 Ala Ile Gln Gly Gly Gln Ile Gly Ile Thr Leu Met Val Arg Trp His
 260 265 270
 Glu Pro Tyr Thr Asp Lys Thr Ala Asp Ala Ala Ala Ile Arg Met
 275 280 285
 Asn Glu Phe His Ile Gly Trp Phe Leu His Pro Leu Val His Gly Asp
 290 295 300
 Tyr Pro Pro Val Met Arg Ser Arg Val Gly Gly Arg Leu Pro Ser Ile
 305 310 315 320
 Thr Ala Ser Asp Ser Glu Lys Ile Arg Gly Ser Phe Asp Phe Ile Gly
 325 330 335
 Ile Asn His Tyr Tyr Val Ile Phe Val Gln Ser Ile Asp Ala Asn Glu
 340 345 350
 Gln Lys Leu Arg Asp Tyr Tyr Ile Asp Ala Gly Val Gln Gly Glu Asp
 355 360 365
 Asp Lys Glu Asn Ile Gln Cys His Ser Trp Ser Leu Gly Lys Val Leu
 370 375 380
 Asn His Leu Lys Leu Glu Tyr Gly Asn Pro Pro Val Met Ile His Glu
 385 390 395 400
 Met Val Ile Gln Ile His Arg Ile Ser Ser Glu Arg Ser Thr Thr Thr
 405 410 415
 Met Thr Ser Asp Arg Ser Ser Cys Arg Ala Thr Trp Lys Leu Cys Ile
 420 425 430
 Cys Pro Tyr Gly Ala Leu Thr Leu Leu Ala Thr Tyr Phe Leu Cys Ala
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 Gly Lys Gly Ser
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<210> 69
 <211> 6282
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> T-DNA sequence
 artificial sequence
 synthetic nucleic acid

<223> synthetic nucleic acid

<400> 69
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